

SRAT

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2004, 18:10:48 ; Search time 19489 Seconds
(without alignments)
7078.910 Million cell updates/sec

Title: US-10-072-077A-1
Perfect score: 3183
Sequence: 1 gatattctttttattatc.....tatgtactagatcgaaattc 3183

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank1:
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2: gb_htg:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	3183	100.0	3183	6 I75096	I75096 Sequence 1
2	3171	99.6	3182	6 AR201516	AR201516 Sequence
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4	2075.8	65.2	59648	8 AB016870	AB016870 Arabidops
5	733.4	23.0	1296	1 TIPMR	K02000 Ti plasmid
6	733.4	23.0	1988	1 ATIMR	X00010 Agrobacteri
7	733.4	23.0	24595	1 ATACH5	X00493 Agrobacteri
8	733.4	23.0	24595	6 E00404	E00404 Ti plasmid
9	733.4	23.0	24595	6 E00546	E00546 DNA fragmen
10	733.4	23.0	24595	6 AR364803	AR364803 Sequence
11	733.4	23.0	24595	6 BD016312	BD016312 Method of
12	733.4	23.0	194140	1 AF242881	AF242881 Agrobacte
13	709	22.3	709	6 I75097	I75097 Sequence 2
14	709	22.3	709	6 AR201517	AR201517 Sequence
15	636.6	20.0	1983	1 ATIMRPTI	X00639 Agrobacteri
16	636.6	20.0	206479	1 AB016260	AB016260 Agrobacte
17	635	19.9	9931	1 AE007927	AE007927 Agrobacte
18	635	19.9	10377	1 AE009419	AE009419 Agrobacte
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21	615.2	19.3	1382	1 PLATIIPTG	X17428 Plasmid Ti
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24	614.4	19.3	14960	1 AVU83986	U83986 Agrobacteri
25	585.8	18.4	2724	1 AB032122	AB032122 Agrobacte
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27	546.6	17.2	1919	1 ABTIIPT	X14410 Agrobacteri
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33	344.4	10.8	584	6 I18499	I18499 Sequence 2
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35	261.8	8.2	4280	6 AX063410	AX063410 Sequence
36	261.8	8.2	4309	6 AX063412	AX063412 Sequence
37	257.2	8.1	1829	6 A26453	A26453 Recombinant
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ALIGNMENTS

RESULT 1
I75096
LOCUS I75096
DEFINITION Sequence 1 from patent US 5689042.
ACCESSION I75096
VERSION I75096.1 GI:3011237
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3183)
AUTHORS Amasino,R.M. and Gan,S.
TITLE Transgenic plants with altered senescence characteristics
JOURNAL Patent: US 5689042-A 1 18-NOV-1997;
FEATURES Location/Qualifiers

Source 1..3183
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 100.0%; Score 3183; DB 6; Length 3183;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AR201516
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DEFINITION Sequence 1 from patent US 6359197.
ACCESSION AR201516
VERSION AR201516.1 GI:20252404
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3182)
AUTHORS Amasino, R.M., Gan, S. and Noh, Y.-S.
TITLE Transgenic plants with altered senescence characteristics
JOURNAL Patent: US 6359197-A 1 19-MAR-2002;
FEATURES
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RESULT 4
AB016870
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (sites)
Asamizu,E., Sato,S., Kaneko,T., Nakamura,Y., Kotani,H., Miyajima,N.
and Tabata,S.
Structural analysis of Arabidopsis thaliana chromosome 5. VIII.
Sequence features of the regions of 1,081,958 bp covered by
seventeen physically assigned P1 and TAC clones
DNA Res. 5 (6), 379-391 (1998)

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Direct Submission
Submitted (18-AUG-1998) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research, 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail: ynakamu@kazusa.or.jp,
Tel: 81-438-52-3935, Fax: 81-438-52-3934)
Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agg_graph.cgi?c=K15122
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlin.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is MR19 and the 3' clone is MC19.

FEATURES
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Db	29576	TTTAGAC-GTTATCACTTCAGCCAAATATGATTTGGATTTAAGTCCAAAATGCAATTCG	29634
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Db	29635	TACGATCCCTCTGTGCTAATGATTTTCAATATTTCTTATATTAATCCCTAATAC	29694
QY	1252	AGAGCTACATTTATTTGTAATCTAATGACAGGAAACCTTTCATAGAGATTCAGATAGAT	1311
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Db	29755	GAATTTGGTGGAAACATCATTTGAACAGAAACCTTTAGCAAAATCATATCGATTTATCTA	29814
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QY	1552	AAAGAAGATTCCTTGTTTTATGTGATTAAGTATTTGATGCAAGAAAGTACCTACGTA	1611
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QY	1612	CTACAAGAAAAATAACATGTACGTACTACGTATCAGCATGTAAAGTATTTTTCGA	1671
Db	30055	CTACAAGAAAAATAACATGTACGTACTACGTATCAGCATGTAAAGTATTTTTCGA	30114
QY	1672	AATAATTTAATCTCATGATAGATTTTTTTTTTGAATGTCAATTAAGAAATGCTTCTT	1731
Db	30115	AATAATTTAATCTCATGATAGATTTTTTTTTTGAATGTCAATTAAGAAATGCTTCTT	30174
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Db	30415	ATGGCTACGTATCAAAACATCAACGATCAATTTAGTTATGTATGAATGAATGTAGTCATTAC	30474
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QY	2092	TCAACCTTATTTTCACTATAAAAACCCATCTCAGTACCTTCTGAGTAATCAAAATTAAG	2151

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QY 2152 AGCAAAAGTCATTAACTTCTCTAAACCATGG 2184
Db 30595 AGCAAAAGTCATTAACTTCTCTAAACCAATGG 30627

RESULT 5

TI6MR 1296 bp DNA linear BCT 13-MAR-1996
LOCUS Ti plasmid (from A.tumefaciens octopine strain) tumor morphology
DEFINITION gene (tmr).

ACCESSION K02000
VERSION K02000.1 GI:154744
KEYWORDS tmr gene; tumor morphology gene.
SOURCE Plasmid Ti
ORGANISM Plasmid Ti

REFERENCE 1 (bases 1 to 1296)
AUTHORS Lichtenstein,C., Klee,H., Montoya,A., Garfinkel,D., Fuller,S.,
Flores,C., Neester,E. and Gordon,M.

TITLE Nucleotide sequence and transcript mapping of the tmr gene of the
PTi6NC octopine Ti-plasmid: a bacterial gene involved in plant
tumorigenesis

JOURNAL J. Mol. Appl. Genet. 2 (4), 354-362 (1984)
MEDLINE 84241512
PubMed 6330262

COMMENT Original source text: Plasmid Ti (clone: pTi6NC.) DNA.

The T-DNA of pTi6NC encodes eight polyadenylated transcripts (see
sites table), and includes at least four genes: tms - tmr - tml -
ocs.

FEATURES

source

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ORIGIN

505 bp upstream of BamHI site.

Query Match 23.0%; Score 733.4; DB 1; Length 1296;
Best Local Similarity 96.0%; Pred. No. 3.1e-106;
Matches 752; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 2139 TAATCAATTAAAGCAAAAGTCATTAACTTCTCTAAACCATGACCCCTGCATCTAAT 2198
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QY 2199 TTTCGGTCCAACTTGACACAGAAAGACGACCGCGATAGCTCTTGCCACAGACAGAG 2258
Db 231 TTTCGGTCCAACTTGACACAGAAAGACGACCGCGATAGCTCTTGCCACAGACAGAG 290

QY 2259 GCTTCCAGTCTTTCGCTTGATCGGCTTCAATCGTGTCTCAACTATCAACCGGAAGCGG 2318
Db 291 GCTTCCAGTCTTTCGCTTGATCGGCTTCAATCGTGTCTCAACTATCAACCGGAAGCGG 350

QY 2319 ACGACCAAGTGAAGAACTGAAGAAAGCAAGCGGCTCTCACTGATGATCGGCTCT 2378
Db 351 ACGACCAAGTGAAGAACTGAAGAAAGCAAGCGGCTCTCACTGATGATCGGCTCT 410

QY 2379 GGTGAGGATATCATCGACGCAAGCAAGCTCATCATAGGCTGATCGAGAGGTATATA 2438
Db 411 GGTGAGGATATCATCGACGCAAGCAAGCTCATCATAGGCTGATCGAGAGGTATATA 470

QY 2439 TCATGAGGCCAACGGCGGCTTATCTTGAGGAGAGATCCACCTGCTCAACTGCAT 2498
Db 471 TCATGAGGCCAACGGCGGCTTATCTTGAGGAGAGATCCACCTGCTCAACTGCAT 530

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QY 2919 GAG 2921
Db 951 GCG 953

RESULT 6

ATTMR 1988 bp DNA linear BCT 12-SEP-1993
LOCUS Agrobacterium tumefaciens tmr-gene encoded by the octopine Ti
DEFINITION Plasmid (tumor inducing).

ACCESSION X00010
VERSION X00010.1 GI:39172
KEYWORDS octopine synthetase; plasmid.
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Agrobacterium tumefaciens
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.

REFERENCE 1 (bases 1 to 1988)
AUTHORS Heidekamp, F., Dirkse, W.G., Hille, J. and van Ormondt, H.
TITLE Nucleotide sequence of the Agrobacterium tumefaciens octopine Ti
JOURNAL plasmid-encoded tmr gene
MEDLINE Nucleic Acids Res. 11 (18), 6211-6223 (1983)
PUBMED 84015366
COMMENT 6312414
The product of the tmr-gene inhibits root formation of the tumors
on certain plant species and appears to play a role in the
cytokinin-independent growth of transformed cells.
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ORIGIN
Query Match 23.0%; Score 733.4; DB 1; Length 1988;
Best Local Similarity 96.0%; Pred. No. 2.9e-106;
Matches 752; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 2139 TAAATCAATTAAGAGCAAAAGTCATTAACTTTCCTAATAAACCATGAGCCCTGCACTTAAT 2198
Db 647 TAAATTAATAAATCAGTTTGTATTCAATATAGTCAAAAAAATTATGAGCCTGCACTTAAT 706
QY 2199 TTTCGGTCCAACTTGACAGAAAGACGACGACCGGATAGCTCTTGCCGACAGACAGG 2258
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Db 767 GCTTCCAGTCCCTTTCGCTTGATCGGGTCCCAATCGTCTCAACTATCAACCGGAAAGCGG 826
QY 2319 ACGACCAACAGTGAAGAACTGAAGAAGACGACGCGTCTTACCTTGATGATCGGCTCT 2378
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QY 2379 GGTGAGGGGTATCATCGCAGCCCAAGCAAGCTCATCATAGGCTGATCGAGAGGTATATA 2438
Db 887 GGTGAGGGGTATCATCGCAGCCCAAGCAAGCTCATCATAGGCTGATCGAGAGGTATATA 946
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Db 1367 AGCCGCTTTCGACGAGATTTCGAAGGTGATCCGTTCCGAAATGTATTAGGTTACGCCAGCCCT 1426
QY 2919 GAG 2921
Db 1427 GCG 1429

RESULT 7
ATACH5 24595 bp DNA linear BCT 10-FEB-1999
LOCUS Agrobacterium tumefaciens Ti plasmid pTi15955 T-DNA region.
DEFINITION X00493 J05108 X00282
ACCESSION X00493 J05108 X00282
VERSION X00493.1 GI:39062
KEYWORDS octopine synthetase; plasmid; synthetase; terminal repeat;
unidentified reading frame.
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Agrobacterium tumefaciens
REFERENCE 1 (bases 1 to 24595)
AUTHORS Barker, R.F., Idler, K.B., Thompson, D.V. and Kemp, J.D.
TITLE Nucleotide sequence of the T-DNA region from the Agrobacterium
tumefaciens octopine Ti plasmid pTi15955
JOURNAL Plant Mol. Biol. 2, 335-350 (1983)
MEDLINE 2 (bases 602 to 14237)
PUBMED 84207942
REFERENCE 3 (bases 1 to 24595)
AUTHORS Turk, S.C., Nester, E.W. and Hooykaas, P.J.
TITLE The virA promoter is a host-range determinant in Agrobacterium
tumefaciens
JOURNAL Mol. Microbiol. 7 (5), 719-724 (1993)
MEDLINE 93225814
PUBMED 8469115
REFERENCE 4 (bases 1 to 24595)
AUTHORS Guevara-Garcia, A., Mosqueda-Cano, C., Arguello-Astorga, G.,
Simpson, J. and Herrera-Estrella, L.
TITLE Tissue-specific and wound-inducible pattern of expression of the
mannopine synthase promoter is determined by the interaction
between positive and negative cis-regulatory elements
JOURNAL Plant J. 4 (3), 495-505 (1993)
MEDLINE 94035196
PUBMED 8220492
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Query Match 23.0%; Score 733.4; DB 1; Length 24595;
Best Local Similarity 96.0%; Pred. No. 2.1e-106;
Matches 752; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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DB	8848	GCTTCCAGTCCCTTTCGCTTGATCGGGTCCAACTGCTCTCAACTATCAACCGGAAGCGG	8907
QY	2319	ACGACCAACAGTGAAGAACTGAAAGAAAGACGCGCTCTCTACCTTGATGATCGGCTCT	2378
DB	8908	ACGACCAACAGTGAAGAACTGAAAGAAAGACGCGCTCTCTACCTTGATGATCGGCTCT	8967
QY	2379	GGTGAGGGGTATCATCGAGCCCAAGCAAGCTCATAGGCTGATCGAGAGGTATATA	2438
DB	8968	GGTGAGGGGTATCATCGAGCCCAAGCAAGCTCATAGGCTGATCGAGAGGTATATA	9027
QY	2439	TCATGAGGCCAACGGCGGCTTATTTCTGAGGAGAGATCCACCTCGTGTCAACTGCAT	2498
DB	9028	TCATGAGGCCAACGGCGGCTTATTTCTGAGGAGAGATCCACCTCGTGTCAACTGCAT	9087
QY	2499	GGCGCGAAACAGCTATTTGAGGTGCAAGATTTTCGTTGGCATAATTATTCGCCACAAGTTACC	2558
DB	9088	GGCGCGAAACAGCTATTTGAGGTGCAAGATTTTCGTTGGCATAATTATTCGCCACAAGTTACC	9147
QY	2559	CGACCAAGAGACCTTCATGAAAGCGGCCAAGGCCAAGGTTAAGCAGATGTTGACCCCGC	2618
DB	9148	CGACCAAGAGACCTTCATGAAAGCGGCCAAGGCCAAGGTTAAGCAGATGTTGACCCCGC	9207
QY	2619	TGCAGGCCATTCTATTATTCAGAGTGTGTTATCTTTGGAATGAACCTCGGCTGAGGCC	2678
DB	9208	TGCAGGCCATTCTATTATTCAGAGTGTGTTATCTTTGGAATGAACCTCGGCTGAGGCC	9267
QY	2679	CATTCTGAAAGAGATCGATGATATGATATGCAATGTTGTTGCTAGCCAGAACAGAT	2738
DB	9268	CATTCTGAAAGAGATCGATGATATGATATGCAATGTTGTTGCTAGCCAGAACAGAT	9327
QY	2739	CACGGCAGATATGCTATTCAGAGCTTGACGCAAAATATGGAAGTTAAGTTAATGGGAT	2798
DB	9328	CACGGCAGATATGCTATTCAGAGCTTGACGCAAAATATGGAAGTTAAGTTAATGGGAT	9387
QY	2799	CGCTCAGAGATTTTCATCCATGCGCGCCCAACAGAGAAAGAAATTCGCCCAAGTTAACGC	2858
DB	9388	CGCTCAGAGATTTTCATCCATGCGCGCCCAACAGAGAAAGAAATTCGCCCAAGTTAACGC	9447
QY	2859	AGCCGCTTTCAGCGGATTCGAAGGTCATCCGTTCCGAATGTATTAGGTTACGCCAGCCCT	2918
DB	9448	AGCCGCTTTCAGCGGATTCGAAGGTCATCCGTTCCGAATGTATTAGGTTACGCCAGCCCT	9507
QY	2919	GAG 2921	
DB	9508	GCG 9510	

RESULT 8
E00404
LOCUS E00404 24595 bp DNA linear PAT 29-SEP-1997

DEFINITION Ti plasmid T-DNA region.
ACCESSION E00404
VERSION E00404.1 GI:2168687
KEYWORDS JP 1985156333-A/1.
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Agrobacterium tumefaciens
REFERENCE 1 (bases 1 to 24595)
AUTHORS Garil,E.D., Denisu,D.S. and Richiyaado,E.B.
TITLE SELECTION USING OPINE SYNTHASE GENE
JOURNAL Patent: JP 1985156333-A 1 16-AUG-1985;
AGURIJENETIKUSU RES ASSOC LTD
COMMENT OS Agrobacterium tumefaciens
PN JP 1985156333-A/1
PD 16-AUG-1985
PE 14-SEP-1984 JP 1984193841
PR 14-SEP-1983 US 83 532280
PI GARIL EE DAARU, DENISU DABURIYU SATSUTON,
PI RICHIAADO EFU BEIKA
PC A01H1/00,C12N5/00,C12N15/00,(C12N5/00,C12R1.91); CC
strandedness: Double;
CC topology: linear;
CC *source: strain=15955;
FH Key Location/Qualifiers

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FT 14060..14083
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/organism="Agrobacterium tumefaciens"
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Query Match 23.0%; Score 733.4; DB 6; Length 24595;
Best Local Similarity 96.0%; Pred. No. 2.1e-106;
Matches 752; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY	2139	TAATCAATTAGAGCAAAAGTCATTACTTCTCTAAACCATGACCCCTGCATCTAAT	2198
DB	8728	TAATATAAAATCAAGTTGTATTCATATACTGCAAAAACCTTATGACCTGCATCTAAT	8787
QY	2199	TTTCGGTCCAACCTTGACAGAGAAAGACGACCGCGATAGCTCTTGCCCAAGACAGAG	2258
DB	8788	TTTCGGTCCAACCTTGACAGAGAAAGACGACCGCGATAGCTCTTGCCCAAGACAGAG	8847
QY	2259	GCTTCCAGTCCCTTTCGCTTGATCGGGTCCAACTGCTCTCAACTATCAACCGGAAGCGG	2318
DB	8848	GCTTCCAGTCCCTTTCGCTTGATCGGGTCCAACTGCTCTCAACTATCAACCGGAAGCGG	8907
QY	2319	ACGACCAACAGTGAAGAACTGAAAGGAAGACGCGCTCTCTACCTTGATGATCGGCTCT	2378
DB	8908	ACGACCAACAGTGAAGAACTGAAAGGAAGACGCGCTCTCTACCTTGATGATCGGCTCT	8967
QY	2379	GGTGAGGGGTATCATCGAGCCCAAGCAAGCTCATAGGCTGATCGAGAGGTATATA	2438
DB	8968	GGTGAGGGGTATCATCGAGCCCAAGCAAGCTCATAGGCTGATCGAGAGGTATATA	9027

QY	2439	TCATGAGGCCAACGGCGGGGCTTATTCTTGAGGGAGATCCACCCTGGTTGCTCAACTGCAT	2498
Db	9028	TCATGAGGCCAACGGCGGGGCTTATTCTTGAGGGAGATCCACCCTGGTTGCTCAACTGCAT	9087
QY	2499	GGCGCGAAACAGCTATTGGAGTGCAGATTTTCGTTGGCATATTATTGCGCCACAAGTTACC	2558
Db	9088	GGCGCGAAACAGCTATTGGAGTGCAGATTTTCGTTGGCATATTATTGCGCCACAAGTTACC	9147
QY	2559	CGACCAAGAGACCTTCATGAAAGCGGCCAAGGCCAGAGTTAAGCAGATGTTGCACCCCGC	2618
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QY	2619	TGCAGGCCATTCTATTATTCAAGAGTTGTTTATCTTTGGAATGAACCTCGGCTGAGCC	2678
Db	9208	TGCAGGCCATTCTATTATTCAAGAGTTGTTTATCTTTGGAATGAACCTCGGCTGAGCC	9267
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Db	9328	CACGCGAGATATGCTATTGCACTTGACGCAATATGGAAGTTAAGTTGATTAATGGAT	9387
QY	2799	CGCTCAGGAGTATTTCATCCATGCGCGCCACACAGAACAGAAATTCGCCCAAGTTAACGC	2858
Db	9388	CGCTCAGGAGTATTTCATCCATGCGCGCCACACAGAACAGAAATTCGCCCAAGTTAACGC	9447
QY	2859	AGCCGCTTTCGACCGGATTCGAAGGTCAATCCGTTCCGAATGTATTAGGTTACGCCAGCCCT	2918
Db	9448	AGCCGCTTTCGACCGGATTCGAAGGTCAATCCGTTCCGAATGTATTAGGTTACGCCAGCCCT	9507
QY	2919	GAG 2921	
Db	9508	GCG 9510	

RESULT	9		
E00546			
LOCUS			
DEFINITION	E00546	24595 bp	DNA linear
ACCESSION	E00546		PAT 29-SEP-1997
VERSION			
KEYWORDS	E00546.1	GI:2168825	
SOURCE	JP 1985256383-A/1.		
ORGANISM	Agrobacterium tumefaciens (Rhizobium radiobacter)		
	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;		
	Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.		
REFERENCE	1 (bases 1 to 24595)		
AUTHORS	Richiyado, E.B. and Jiyon, D.K.		
TITLE	PROMOTOR OF OCTOPINE T-DNA		
JOURNAL	Patent: JP 1985256383-A 1 18-DEC-1985;		
	AGURIJENETEIKUSU RES ASSOC LTD		
COMMENT	OS Agrobacterium tumefaciens		
	PN JP 1985256383-A/1		
	PD 18-DEC-1985		
	PF 19-NOV-1984 JP 1984244307		
	PR 18-NOV-1983 US 83 553786		
	PI RICHYADO EFU BEIKA, JIYON DEI KENPU		
	PC C12N15/00,A01H1/00,C12N1/20,C12N5/00//C07H21/04,(C12N1/20, PC		
	C12R1:01),		
	PC (C12N5/00,C12R1:91);		
	CC strandedness: Single;		
	CC topology: Linear;		
	CC hypothetical: No;		
	CC anti-sense: No;		
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		1. .24595
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ORIGIN

Query Match	23.0%	Score 733.4;	DB 6;	Length 24595;
Best Local Similarity	96.0%;	Pred. No. 2.1e-106;		
Matches 752; Conservative	0;	Mismatches 31;	Indels 0;	Gaps 0;

QY	2139	TAATCAAAATTAGAGCAAAAAGTCATTTAACCTTCTTAAACCATGACCCCTGATCTAAT	2198
Db	8728	TAATATAAAAAATCAGTTTGTATTCAATATATACGAAAAAACTTATGACCTGATCTAAT	8787
QY	2199	TTTCGGTCCAACTTGCA CAGGAAAGACGACGCCGATAGCTCTTGCCACAGACAGG	2258
Db	8788	TTTCGGTCCAACTTGCA CAGGAAAGACGACGCCGATAGCTCTTGCCACAGACAGG	8847
QY	2259	GCTTCAGTCCCTTCGCTTGATCGGCTCCAAATCGTGTCCTCAACTATCAACCGGAACGG	2318
Db	8848	GCTTCAGTCCCTTCGCTTGATCGGCTCCAAATGCTGTCTCAACTATCAACCGGAACGG	8907
QY	2319	ACGACCAACAGTGGAGAACA CTGAAAGGAACGACGCCGCTCTA CTTGATGATCGGCTCT	2378
Db	8908	ACGACCAACAGTGGAGAACA CTGAAAGGAACGACGCCGCTCTA CTTGATGATCGGCTCT	8967
QY	2379	GGTGGAGGGTATCATCGCAGCCCAAGCAAGCTCATCATAGGCTGATCGAGGAGGTGATAA	2438
Db	8968	GGTGGAGGGTATCATCGCAGCCCAAGCAAGCTCATCATAGGCTGATCGAGGAGGTGATAA	9027
QY	2439	TCATGAGGCCAAACGGCGGCTTATCTTGAGGGAGATCCACCTCGTTGCTCAACTGCAT	2498
Db	9028	TCATGAGGCCAAACGGCGGCTTATCTTGAGGGAGATCCACCTCGTTGCTCAACTGCAT	9087
QY	2499	GGCGCGAAACAGCTAATTGAGTGCAGATTTTCGTGGCATATTATTGCGCCACAAGTTAAC	2558
Db	9088	GGCGCGAAACAGCTAATTGAGTGCAGATTTTCGTGGCATATTATTGCGCCACAAGTTAAC	9147
QY	2559	CGACCAAGAGACCTTCATGGAAGCGGCCAAGGCCAGATTAAAGCAGATGTTGCACCCCGC	2618
Db	9148	CGACCAAGAGACCTTCATGGAAGCGGCCAAGGCCAGATTAAAGCAGATGTTGCACCCCGC	9207
QY	2619	TGCAGGCCATTCTAATTATTCAAGAGTGGTTTATCTTTGGAATGAACCTCGGCTGAGGCC	2678
Db	9208	TGCAGGCCATTCTAATTATTCAAGAGTGGTTTATCTTTGGAATGAACCTCGGCTGAGGCC	9267
QY	2679	CATTCTGAAGAGATCGATGGATATCGATATGCCATGTTGTTGCTAGCCAGAACCAAGAT	2738
Db	9268	CATTCTGAAGAGATCGATGGATATCGATATGCCATGTTGTTGCTAGCCAGAACCAAGAT	9327
QY	2739	CACGCGAGATATGCTAATTGCACTTGACGCAAAATATGGAAGGTAAGTTGATTAAATGGGAT	2798
Db	9328	CACGCGAGATATGCTAATTGCACTTGACGCAAAATATGGAAGGTAAGTTGATTAAATGGGAT	9387
QY	2799	CGCTCAGAGTATTTCAATCCATGCGCGCAACAGACAGAAATTCCCCCAAGTTAAAGC	2858
Db	9388	CGCTCAGAGTATTTCAATCCATGCGCGCAACAGACAGAAATTTCCCCCAAGTTAAAGC	9447
QY	2859	AGCCGCTTTGACCGGATTCGAAGGTCATCCGTTCCGAATGTATTAGGTTACGCCAGCCCT	2918
Db	9448	AGCCGCTTTGACCGGATTCGAAGGTCATCCGTTCCGAATGTATTAGGTTACGCCAGCCCT	9507
QY	2919	GAG 2921	
Db	9508	GCG 9510	

RESULT 10

AR364803 AR364803 24595 bp DNA linear PAT 03-SEP-2003
LOCUS AR364803
DEFINITION Sequence 1 from patent US 5428147.
ACCESSION AR364803
VERSION AR364803.1 GI:34427834
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 24595)
AUTHORS Barker,R.F. and Kemp,J.D.
TITLE Octopine T-DNA promoters
JOURNAL Patent: US 5428147-A 1 27-JUN-1995;
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source 1. .24595
/organism="unknown"
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ORIGIN
Query Match 23.0%; Score 733.4; DB 6; Length 24595;
Best Local Similarity 96.0%; Pred. No. 2.1e-106;
Matches 752; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 2139 TAATCAATTAAAGCAAAAGTCATTTAACTTTCTAAACCATGAGCCCTGCATCTAAT 2198
DB 8728 TAATATAAAATCAGTTTGTATTCATATACTGCAGAAAACTTATGACCTGCATCTAAT 8787
QY 2199 TTTCGGTCCACTTGCACAGAAAGACGACGCGGATAGCTCTTGCCGACAGACAGG 2258
DB 8788 TTTCGGTCCACTTGCACAGAAAGACGACGCGGATAGCTCTTGCCGACAGACAGG 8847
QY 2259 GCTTCCAGTCTTTCGCTTGATCGGGTCCATCGTCTCTCACTATCAACCGGAAGCGG 2318
DB 8848 GCTTCCAGTCTTTCGCTTGATCGGGTCCATCGTCTCTCACTATCAACCGGAAGCGG 8907
QY 2319 AGCACCAACAGTGAAGAACTGAAAGGAACGACGCGTCTCTAACCCTGATGATCGGCTCT 2378
DB 8908 AGCACCAACAGTGAAGAACTGAAAGGAACGACGCGTCTCTAACCCTGATGATCGGCTCT 8967
QY 2379 GGTGAGGGTATCATCGACGCCAAGCAAGCTCATATAGGCTGATCGAGGAGGTATTA 2438
DB 8968 GGTGAGGGTATCATCGACGCCAAGCAAGCTCATATAGGCTGATCGAGGAGGTATTA 9027
QY 2439 TCATGAGGCCAAGCGGCTTATTTCTTGAGGAGGATCCACCTGCTGCTCAATGCAAT 2498
DB 9028 TCATGAGGCCAAGCGGCTTATTTCTTGAGGAGGATCCACCTGCTGCTCAATGCAAT 9087
QY 2499 GGGCGAAGACAGCTATTTGAGTGCAGATTTTCTTGCGCATATTATTCGCCACAAGTTAAC 2558
DB 9088 GGGCGAAGACAGCTATTTGAGTGCAGATTTTCTTGCGCATATTATTCGCCACAAGTTAAC 9147
QY 2559 CGACCAAGACAGCTTCATGAAGCGGCCAAGGCCAGAGTTAAGCAGATGTTGACCCCGC 2618
DB 9148 CGACCAAGACAGCTTCATGAAGCGGCCAAGGCCAGAGTTAAGCAGATGTTGACCCCGC 9207
QY 2619 TGCAGGCCATTTATATTCAAGAGTTGTTTATTTTGAATGAACCTCGGCTGAGGCC 2678
DB 9208 TGCAGGCCATTTATATTCAAGAGTTGTTTATTTTGAATGAACCTCGGCTGAGGCC 9267
QY 2679 CATTTGAAAAGATCGATGATATGATATGCCATGTTGTTGCTAGCCAGAACCAAT 2738
DB 9268 CATTTGAAAAGATCGATGATATGATATGCCATGTTGTTGCTAGCCAGAACCAAT 9327
QY 2739 CACGGCAGATATGCTATTGACGCTGACGCAATATGGAAGGTAAGTTAATGGAT 2798
DB 9328 CACGGCAGATATGCTATTGACGCTGACGCAATATGGAAGGTAAGTTAATGGAT 9387
QY 2799 CGCTCAGAGTATTTTCATCATGCGCGGCCAACAGAACAGAAATTCGCCCAAGTTAACGC 2858
DB 9388 CGCTCAGAGTATTTTCATCATGCGCGGCCAACAGAACAGAAATTCGCCCAAGTTAACGC 9447
QY 2859 AGCGGCTTTCAGCGGATTCGAAGGTCAATCCGTTTCCGAATGATTAAGTTAGCCAGCCCT 2918

DB 9448 AGCGGCTTTCAGCGGATTCGAAGGTCAATCCGTTTCCGAATGATTAAGTTAGCCAGCCCT 9507
QY 2919 GAG 2921
DB 9508 GCG 9510
RESULT 11
BD016312 24595 bp DNA linear PAT 27-AUG-2002
LOCUS BD016312
DEFINITION Method of promoting plant transcription by using octopine T-DNA
promoter.
ACCESSION BD016312
VERSION BD016312.1 GI:22557450
KEYWORDS JP 2001190289-A/1.
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Agrobacterium tumefaciens
REFERENCE 1 (bases 1 to 24595)
AUTHORS Barker,R.F. and Kemp,J.D.
TITLE Method of promoting plant transcription by using octopine T-DNA
JOURNAL Patent: JP 2001190289-A 1 17-JUL-2001;
COMMENT MYCOGEN PLANT SCIENCE INC
OS Agrobacterium tumefaciens
PN JP 2001190289-A/1
PD 17-JUL-2001
PF 22-NOV-2000 JP 2000356816
PR 18-NOV-1983 US 553786
PI RICHARD F BARKER,JOHN D KEMP
PC C12N15/09,A01H5/00,C12N5/10,C12N15/00,C12N5/00 CC Method of
promoting plant transcription by using octopine T- CC
DNA Promoter
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ORIGIN
Query Match 23.0%; Score 733.4; DB 6; Length 24595;
Best Local Similarity 96.0%; Pred. No. 2.1e-106;
Matches 752; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 2139 TAATCAATTAAAGCAAAAGTCATTTAACTTTCTAAACCATGAGCCCTGCATCTAAT 2198
DB 8728 TAATATAAAATCAGTTTGTATTCATATACTGCAGAAAACTTATGAGCCTGCATCTAAT 8787
QY 2199 TTTCGGTCCACTTGCACAGAAAGACGACGCGGATAGCTCTTGCCGACAGACAGG 2258
DB 8788 TTTCGGTCCACTTGCACAGAAAGACGACGCGGATAGCTCTTGCCGACAGACAGG 8847
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QY 2319 AGCACCAACAGTGAAGAACTGAAAGGAACGACGCGTCTCTACCTGATGATCGGCTCT 2378
DB 8908 AGCACCAACAGTGAAGAACTGAAAGGAACGACGCGTCTCTACCTGATGATCGGCTCT 8967
QY 2379 GGTGAGGGTATCATCGACGCCAAGCAAGCTCATAGGCTGATCGAGGAGGTATTA 2438
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QY 2439 TCATGAGGCCAAGCGGCTTATTTCTTGAGGAGGATCCACCTCGTTGCTCAACTGCAT 2498
DB 9028 TCATGAGGCCAAGCGGCTTATTTCTTGAGGAGGATCCACCTCGTTGCTCAACTGCAT 9087
QY 2499 GGGCGAAGACAGCTATTTGAGTGCAGATTTTCTTGCGCATATTATTCGCCACAAGTTAAC 2558

Db 9088 GGGCGGAAACAGCTATTGGAGTGCAGATTTTCGTTGGCATATTATTCGCCACAAGTTACC 9147

QY 2559 CGACCAAGAGACCTTCATGAAAGCGGCCAAGGCCAGAGTTAAGCATGTTGCACCCCGC 2618

Db 9148 CGACCAAGAGACCTTCATGAAAGCGGCCAAGGCCAGAGTTAAGCATGTTGCACCCCGC 9207

QY 2619 TGCAGGCCATTCTATTATTCAGAGTTGGTTTATCTTTGGAATGAACCTCGGCTGAGGCC 2678

Db 9208 TGCAGGCCATTCTATTATTCAGAGTTGGTTTATCTTTGGAATGAACCTCGGCTGAGGCC 9267

QY 2679 CATTTGAAAGAGATCGATGGATATGCATATGCCATGTTGTTGCTAGCCAGAACCAAGAT 2738

Db 9268 CATTTGAAAGAGATCGATGGATATGCATATGCCATGTTGTTGCTAGCCAGAACCAAGAT 9327

QY 2739 CACGGCAGATATGCTATTGACGCTTGACGCAATATGGAAGTTAGTTAATGGGAT 2798

Db 9328 CACGGCAGATATGCTATTGACGCTTGACGCAATATGGAAGTTAGTTAATGGGAT 9387

QY 2799 CGCTCAGAGATATTTTCATCCATGCGCGCCCAACAGACAGAAATTCGCCCAAGTTAAAGC 2858

Db 9388 CGCTCAGAGATATTTTCATCCATGCGCGCCCAACAGACAGAAATTCGCCCAAGTTAAAGC 9447

QY 2859 AGCCGCTTTTCGACGGATTCGAGGTGATCCGTTCCGAATGTAATTAGTTACGCCAGCCCT 2918

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QY 2919 GAG 2921

Db 9508 GCG 9510

RESULT 12

AF242881 194140 bp DNA circular BCT 26-JUN-2000

LOCUS AF242881 Agrobacterium tumefaciens octopine-type Ti plasmid, complete sequence.

DEFINITION

ACCESSION AF242881 AF034854 AF034855 AF035413 AF035773 AF039887 AF039888 AF117204 AH006976 M14480 M14762 M80605 M80607 U19620 U43674 U43675 U48718 U60011 X04784

VERSION AF242881.1 GI:8572673

KEYWORDS Agrobacterium tumefaciens (Rhizobium radiobacter)

SOURCE Agrobacterium tumefaciens

ORGANISM Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.

REFERENCE 1 (bases 193234 to 194140; 1 to 23692) Barker, R.F., Idler, K.B., Thompson, D.V. and Kemp, J.D. Nucleotide sequence of the T-DNA region from the Agrobacterium tumefaciens octopine Ti plasmid pTi15955

JOURNAL Plant Mol. Biol. 2, 335-350 (1983)

REFERENCE 2 (bases 166443 to 168193) Yanofsky, M.F. and Nester, E.W. Molecular characterization of a host-range-determining locus from Agrobacterium tumefaciens

JOURNAL J. Bacteriol. 168 (1), 244-250 (1986)

MEDLINE 87008387

PUBMED 3759904

REFERENCE 3 (bases 168089 to 173951) Yanofsky, M.F., Porter, S.G., Young, C., Albright, L.M., Gordon, M.P. and Nester, E.W. The virD operon of Agrobacterium tumefaciens encodes a site-specific endonuclease

JOURNAL Cell 47 (3), 471-477 (1986)

MEDLINE 87028239

PUBMED 3021341

REFERENCE 4 (bases 175278 to 177719) Winans, S.C., Allenza, P., Stachel, S.E., McBride, K.E. and Nester, E.W. Characterization of the virE operon of the Agrobacterium Ti plasmid pTiA6

JOURNAL Nucleic Acids Res. 15 (2), 825-837 (1987)

MEDLINE 87146396

PUBMED 3547330

REFERENCE 5 (bases 50125 to 54471) Habeeb, L.F., Wang, L. and Winans, S.C. Transcription of the octopine catabolism operon of the Agrobacterium tumor-inducing plasmid pTiA6 is activated by a LysR-type regulatory protein

JOURNAL Mol. Plant Microbe Interact. 4 (4), 379-385 (1991)

MEDLINE 92190631

PUBMED 1799699

REFERENCE 6 (bases 50125 to 54471) Valdivia, R.H., Wang, L. and Winans, S.C. Characterization of a putative periplasmic transport system for octopine accumulation encoded by Agrobacterium tumefaciens Ti plasmid pTiA6

JOURNAL J. Bacteriol. 173 (20), 6398-6405 (1991)

MEDLINE 92011411

PUBMED 1655707

REFERENCE 7 (bases 68024 to 76460) Kim, K.S. and Farrand, S.K. Ti plasmid-encoded genes responsible for catabolism of the crown gall opine mannopine by Agrobacterium tumefaciens are homologs of the T-region genes responsible for synthesis of this opine by the plant tumor

JOURNAL J. Bacteriol. 178 (11), 3275-3284 (1996)

MEDLINE 96236046

PUBMED 8655509

REFERENCE 8 (bases 39167 to 45466) Fuqua, C. and Winans, S.C. Localization of OccR-activated and Trar-activated promoters that express two ABC-type permeases and the trar gene of Ti plasmid pTiR10

JOURNAL Mol. Microbiol. 20 (6), 1199-1210 (1996)

MEDLINE 96405643

PUBMED 8809772

REFERENCE 9 (bases 22855 to 39243; 96353 to 111409) Alt-Morbe, J., Stryker, J.L., Fuqua, C., Li, P.L., Farrand, S.K. and Winans, S.C. The conjugal transfer system of Agrobacterium tumefaciens octopine-type Ti plasmids is closely related to the transfer system of an IncP plasmid and distantly related to Ti plasmid vir genes

JOURNAL J. Bacteriol. 178 (14), 4248-4257 (1996)

MEDLINE 96312368

PUBMED 8763954

REFERENCE 10 (bases 54312 to 62806) Oger, P., Kim, K.S., Sackett, R.L., Piper, K.R. and Farrand, S.K. Octopine-type Ti plasmids code for a mannopine-inducible dominant-negative allele of trar, the quorum-sensing activator that regulates Ti plasmid conjugal transfer

JOURNAL Mol. Microbiol. 27 (2), 277-288 (1998)

MEDLINE 98143415

PUBMED 9484884

REFERENCE 11 (bases 133963 to 138972) Kalogeraki, V.S. and Winans, S.C. Wound-released chemical signals may elicit multiple responses from an Agrobacterium tumefaciens strain containing an octopine-type Ti plasmid

JOURNAL J. Bacteriol. 180 (21), 5660-5667 (1998)

MEDLINE 99009000

PUBMED 9791116

REFERENCE 12 (bases 76455 to 98723) Lyi, S.M., Jafri, S. and Winans, S.C. Mannopinic acid and agropinic acid catabolism region of the octopine-type Ti plasmid pTi15955

JOURNAL Mol. Microbiol. 31 (1), 339-347 (1999)

MEDLINE 99141607

PUBMED 9987134

REFERENCE 13 (bases 1 to 194140) Winans, S.C., Zhu, J., Oger, P.M., Schrammeijer, B., Hoojkaas, P.J. and Farrand, S.K. Octopine-type Ti plasmid sequence

JOURNAL Unpublished

REFERENCE 14 (bases 68024 to 76460) Kim, K.-S. Direct Submission

JOURNAL Submitted (10-JAN-1995) Kun-Soo Kim, Microbiology, University of Illinois at Urbana-Champaign, 1201 W. Gregory Dr., Urbana, IL 61801, USA

REFERENCE 15 (bases 96353 to 111409)

AUTHORS Winans,S.C.

TITLE Direct Submission

JOURNAL Submitted (20-DEC-1995) Stephen C. Winans, Microbiology, Cornell University, Wing Hall, Ithaca, NY 14853, USA

REFERENCE 16 (bases 39167 to 45466)

AUTHORS Fuqua,C.

TITLE Direct Submission

JOURNAL Submitted (07-FEB-1996) Clay Fuqua, Biology, Trinity University, 715 Stadium Dr., San Antonio, TX 78212, USA

REFERENCE 17 (bases 54312 to 62806)

AUTHORS Kim,K.-S., Sackett,R.L. and Farrand,S.K.

TITLE Direct Submission

JOURNAL Submitted (04-JUN-1996) Crop Sciences, University of Illinois at Urbana-Champaign, 240 ERMU, 1201 W. Gregory Dr., Urbana, IL 61801, USA

REFERENCE 18 (bases 186239 to 193239)

AUTHORS Zhu,J. and Winans,S.C.

TITLE Direct Submission

JOURNAL Submitted (17-NOV-1997) Section of Microbiology, Cornell University, Wing Hall, Ithaca, NY 14853, USA

REFERENCE 19 (bases 76455 to 98723)

AUTHORS Winans,S.C. and Lyi,S.

TITLE Direct Submission

JOURNAL Submitted (20-NOV-1997) Microbiology, Cornell University, Wing Hall, Ithaca, NY 14853, USA

REFERENCE 20 (bases 170209 to 175283)

AUTHORS Zhu,J. and Winans,S.C.

TITLE Direct Submission

JOURNAL Submitted (25-NOV-1997) Section of Microbiology, Cornell University, Wing Hall, Ithaca, NY 14853, USA

REFERENCE 21 (bases 133963 to 138972; 176911 to 186244)

AUTHORS Styker,J.L., Mantis,N.J., Kalogeraki,V.S. and Winans,S.C.

TITLE Direct Submission

JOURNAL Submitted (23-DEC-1997) Microbiology, Cornell University, Ithaca, NY 14853, USA

REFERENCE 22 (bases 22855 to 39243)

AUTHORS Winans,S.C.

TITLE Direct Submission

JOURNAL Submitted (03-AUG-1998) Microbiology, Cornell University, Wing Hall, Ithaca, NY 14853, USA

REFERENCE 23 (bases 62801 to 66985)

AUTHORS Oger,P.M.

TITLE Direct Submission

JOURNAL Submitted (29-DEC-1998) Crop Sciences, University of Illinois at Urbana-Champaign, 361 ERMU, 1201, W. Gregory Dr., Urbana, IL 61801, USA

REFERENCE 24 (bases 110822 to 133968)

AUTHORS Zhu,J. and Winans,S.C.

TITLE Direct Submission

JOURNAL Submitted (18-AUG-1999) Section of Microbiology, Cornell University, Wing Hall, Ithaca, NY 14853, USA

REFERENCE 25 (bases 1 to 194140)

AUTHORS Zhu,J., Oger,P.M., Schrammeijer,B., Hooymaas,P.J., Farrand,S.K. and Winans,S.C.

TITLE Direct Submission

JOURNAL Submitted (07-MAR-2000) Microbiology, Cornell University, Wing Hall, Ithaca, NY 14853, USA

COMMENT On or before Jun 20, 2000 this sequence version replaced gi:3377769, gi:1215729, gi:1381799, gi:797330, gi:2665704, gi:2749889, gi:5738260, gi:2773254, gi:2773255, gi:2773256, gi:154820, gi:154827, gi:2662524, gi:39122, gi:2687604, gi:154767, gi:154773, gi:6689862.

FEATURES Location/Qualifiers

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DEFINITION	Sequence 2 from patent US 5689042.								
ACCESSION	175097								
VERSION	175097.1	GI:3011238							
KEYWORDS									
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	1 (bases 1 to 709)								
AUTHORS	Amasino, R.M. and Gan, S.								
TITLE	Transgenic plants with altered senescence characteristics								
JOURNAL	Patent: US 5689042-A 2 18-NOV-1997;								
FEATURES	Location/Qualifiers								
source	1. 709								
ORIGIN									
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Best Local Similarity	100.0%;	Pred. No. 2.4e-102;							
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QY	1592	GCATGAAGGTACCTACGTAAGAAATAAATTAACATGTACGTAACGTAACGCA	1651						
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QY	1652	TGTAAAGATTTTTTCCAAATAATTTAATCAATGATGATGATTTTTTTTGAATG	1711						
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Db	481	CAGTTGATGAGGACTAAATGGCTACGATCAAAACATCAACGATCATTTAGTTATGTA	540						
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ACCESSION	AR201517								
VERSION	AR201517.1	GI:20252405							
KEYWORDS									
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	1 (bases 1 to 709)								
AUTHORS	Amasino, R.M., Gan, S. and Noh, Y.-S.								
TITLE	Transgenic plants with altered senescence characteristics								
JOURNAL	Patent: US 6359197-A 2 19-MAR-2002;								
FEATURES	Location/Qualifiers								
source	1. 709								
ORIGIN									
Query Match	22.3%;	Score 709;	DB 6;	Length 709;					
Best Local Similarity	100.0%;	Pred. No. 2.4e-102;							
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DEFINITION X00639
VERSION X00639.1 GI:944822
KEYWORDS cytotoxin; plasmid.
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Agrobacterium tumefaciens
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
REFERENCE 1 (bases 1 to 1982)
AUTHORS Goldberg, S.B., Flick, J.S. and Rogers, S.G.
TITLE Nucleotide sequence of the tmr locus of Agrobacterium tumefaciens
PTi T37 T-DNA
JOURNAL Nucleic Acids Res. 12 (11), 4665-4677 (1984)
MEDLINE 84247329
PUBMED 6330678
COMMENT On Aug 15, 1995 this sequence version replaced gi:39174.
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TATA_signal 588..592
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ORIGIN polya_signal 1418..1422

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Best Local Similarity 90.8%; Pred. No. 5.7e-91;
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QY 2295 TCCTCAACTATCAACCGGAGCGGACGACCAACAGTGAAGAACTGAAAGGAAAGGACGCG 2354
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QY 2355 TCTCTAAGCTGATGATCGGCTCTGCTGAGGGTATCATCGCAGCCAAAGCTCATCA 2414
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QY 2475 ATCCACCTGCTGCTCAACTGCATGGCGGAAACAGCTATGAGTGCAGATTTTCTTG 2534
Db 952 ATCTATCTGCTGCTCAAGTGCATGGCGGAAACAGCTATGAGTGCAGATTTTCTTG 1011

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Db 1372 AATGTAATGAGTTACGCCACGCGCTGAG 1398

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-10-072-077A-1

Perfect score: 3183
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Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	3171	99.6	3182	6 AAD33336	Aad33336 A. thalia
4	734.8	23.1	745	2 AAV69757	Aav69757 Isopenten
5	733.4	23.0	1988	6 ABK12492	Abk12492 Agrobacte
6	733.4	23.0	24596	1 AAN50182	Aan50182 Complete
7	730.2	22.9	24593	1 AAN50226	Aan50226 Sequence
8	714.8	22.5	723	3 AAD00619	Aad00619 Agrobacte
9	712.2	22.4	747	3 AAD00624	Aad00624 Agrobacte
10	709	22.3	709	2 AAT42917	Aat42917 SAG12-1 p
11	709	22.3	709	6 AAD33337	Aad33337 Arabidops
12	701.2	22.0	723	1 AAN70790	Aan70790 Sequence
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22	262.8	8.3	7599	4 AAF25320	Aaf25320 Nucleotid
23	261.8	8.2	4280	4 AAF25317	Aaf25317 Nucleotid

24	261.8	8.2	4309	4 AAF25319	Aaf25319 Nucleotid
25	257.2	8.1	1829	2 AAQ29293	Aaq29293 35S CamV
26	257.2	8.1	1863	2 AAQ21191	Aaq21191 Sequence
27	257.2	8.1	1863	2 AAQ74261	Aaq74261 Tomato-to
28	257.2	8.1	4284	2 AAQ74259	Aaq74259 Stress-in
29	256.2	8.0	12982	4 AAF86432	Aaf86432 Vector ps
30	256.2	8.0	15397	2 AAT58635	Aat58635 T-DNA ins
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32	256	8.0	5534	2 AAT43137	Aat43137 pUMIGIT s
33	255.8	8.0	5465	2 AAZ20088	Aaz20088 Plasmid p
34	255.6	8.0	17458	2 ABQ82142	Abq82142 Acceptor
35	255.6	8.0	17476	6 ABQ82141	Abq82141 Acceptor
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38	255.2	8.0	8074	6 ABA05262	Abao5262 Plasmid p
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41	255	8.0	6548	2 AAT61394	Aat61394 Plasmid p
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44	254.2	8.0	2709	2 AAV44284	Aav44284 Oleosin-p
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ALIGNMENTS

RESULT 1
ID AAT42919 standard; DNA; 3183 BP.
XX
AC AAT42919;
XX
DT 18-JAN-1997 (first entry)
XX
DE SAG12-1 Promoter, isopentenyltransferase gene and NOS terminator.
XX
KW SAG12-1; promoter; senescence-associated gene; isopentenyltransferase;
KW NOS terminator; Arabidopsis thaliana; development; gene regulation;
KW 5'-untranslated region; cytokinin biosynthesis; transgenic plant;
KW flowering; seed; fruit; crop improvement; ds.
XX
OS Arabidopsis thaliana.
XX
FH Key location/Qualifiers
XX
FH promoter 1..2073
FT FT /*tag= a
FT FT 1473..2073
FT FT /*tag= b
FT FT /note= "Truncated promoter (AAT42917, claim 2)"
FT FT 5'UTR 2074..2180
FT FT /*tag= c
FT FT CDS 2181..2920
FT FT /*tag= d
FT FT /product= "Isopentenyltransferase"
FT FT 2921..3180
FT FT /*tag= e
FT FT /note= "NOS terminator"
XX
PN WO9629858-A1.
XX
PD 03-OCT-1996.
XX
XX 20-FEB-1996; 96WO-US002313.
XX
XX 29-MAR-1995; 95US-00413135.
XX
XX (WISC) WISCONSIN ALUMNI RES FOUND.
XX
XX Amasino RM, Gan S;
XX
XX WPI; 1996-454877/45.

PT Senescence associated gene promoters, SAG12 and SAG13, - useful for
PT producing genetic constructs for producing transgenic plants having
PT delayed senescence.

XX Example; Page 26-27; 38pp; English.

CC The sequence represents a full-length version of the SAG12-1 promoter
CC (truncated version given in AAT42917) from an Arabidopsis thaliana
CC senescence-associated gene. The sequence also contains the SAG12-1 gene
CC 5'-untranslated region, and has been linked to a cytokinin biosynthesis
CC isopentenyltransferase gene and NOS terminator for senescence-specific
CC gene expression in a transgenic plant. The resulting transgenic plant
CC shows delayed senescence, and shows longer vegetative growth, producing
CC more flowers, seeds or fruit

XX Sequence 3183 BP; 1042 A; 527 C; 560 G; 1054 T; 0 U; 0 Other;

Query Match 100.0%; Score 3183; DB 2; Length 3183;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATATCTCTTTTATATTCAAACAATAAGTGAATGTTGAGAGAGACAATATT 60
DB 1 GATATCTCTTTTATATTCAAACAATAAGTGAATGTTGAGAGAGACAATATT 60
QY 61 CTCGTGAGCACCAGCTCTGTTTATATAGAAACCCGATTGTTATTTTAGACTGAGAC 120
DB 61 CTCGTGAGCACCAGCTCTGTTTATATAGAAACCCGATTGTTATTTTAGACTGAGAC 120
QY 121 AAAAAAGTAAATCGTTGATTGTTAAATTTAAATTTAGTTTCATCAGCTTCGATAAA 180
DB 121 AAAAAAGTAAATCGTTGATTGTTAAATTTAAATTTAGTTTCATCAGCTTCGATAAA 180
QY 181 AAATGATTAGTATCATAGCTAATATAGCAATGATTCTAAATTTGTTTGAACACCTTT 240
DB 181 AAATGATTAGTATCATAGCTAATATAGCAATGATTCTAAATTTGTTTGAACACCTTT 240
QY 241 TTTCTCTCTTGTGTTTCTTAAACATTAGAGAACCCATAACATGTACGTTCAAAAT 300
DB 241 TTTCTCTCTTGTGTTTCTTAAACATTAGAGAACCCATAACATGTACGTTCAAAAT 300
QY 301 AATTAACCAATATTTCCAGTTTATATAGCAAACTGTTTTTAAATGAACAAGTT 360
DB 301 AATTAACCAATATTTCCAGTTTATATAGCAAACTGTTTTTAAATGAACAAGTT 360
QY 361 GAATAGTGTATGATTAATAGTATGATCAATCTCAATATATGATCAATGATGTATAT 420
DB 361 GAATAGTGTATGATTAATAGTATGATCAATCTCAATATATGATCAATGATGTATAT 420
QY 421 ATGAACTCAGTTGTATACAGAAATGAATAATGCTATTTAAATACCGATCATGAAGTT 480
DB 421 ATGAACTCAGTTGTATACAGAAATGAATAATGCTATTTAAATACCGATCATGAAGTT 480
QY 481 AAAAAAGTGCAGATATGACATGAGCGTTTGTCTACCGGGTATCGAGTTATAGTTT 540
DB 481 AAAAAAGTGCAGATATGACATGAGCGTTTGTCTACCGGGTATCGAGTTATAGTTT 540
QY 541 GGATCTCTCAAGATATTTGGCCATATAGTATATTTGGCCTTAAGCGTTTGCATA 600
DB 541 GGATCTCTCAAGATATTTGGCCATATAGTATATTTGGCCTTAAGCGTTTGCATA 600
QY 601 GAGACGAGAGAAAGATTTGGGTCAAGTTTAAACAAACAGAGACCTCGTATTAGTTGTA 660
DB 601 GAGACGAGAGAAAGATTTGGGTCAAGTTTAAACAAACAGAGACCTCGTATTAGTTGTA 660
QY 661 CTTTGGTAGCAAGTCGATTATTTGCCAGTAAAACTTGGTACACAACCTGACAACCTGTA 720
DB 661 CTTTGGTAGCAAGTCGATTATTTGCCAGTAAAACTTGGTACACAACCTGACAACCTGTA 720
QY 721 TCGTTATTAGTTTGTACTTGTGACCTTTGGTTAAGAAAAAGTTGATATAGTTAATCAGT 780
DB 721 TCGTTATTAGTTTGTACTTGTGACCTTTGGTTAAGAAAAAGTTGATATAGTTAATCAGT 780

QY 781 TGTGTTTCATGAGGTGATGTTAATTTGTTGACTAGGGCGATTCTTCACATACAA 840
DB 781 TGTGTTTCATGAGGTGATGTTAATTTGTTGACTAGGGCGATTCTTCACATACAA 840
QY 841 TAACAAAGTTTATAGATTTTTTTTATACATTTTCCACGCTTCGTAAGTTGGTA 900
DB 841 TAACAAAGTTTATAGATTTTTTTTATACATTTTCCACGCTTCGTAAGTTGGTA 900
QY 901 TTACACCCGATTTTCCCTGTAACAAGATTCATATATTTATATATCTCCAGTT 960
DB 901 TTACACCCGATTTTCCCTGTAACAAGATTCATATATTTATATATCTCCAGTT 960
QY 961 GACAATTATAGTTTATACGTTTTTACAATTATTTAAATACCATGTGAAGATCCAAGAA 1020
DB 961 GACAATTATAGTTTATACGTTTTTACAATTATTTAAATACCATGTGAAGATCCAAGAA 1020
QY 1021 TATGCTTACTCTCTTGTGTAAGAAAACTAATATATCTATATTAATAATATCT 1080
DB 1021 TATGCTTACTCTCTTGTGTAAGAAAACTAATATATCTATATTAATAATATCT 1080
QY 1081 AATCATATATTTGTAATATAGCAATTTGTCATATTTGAATTTAGTATTTAGACGG 1140
DB 1081 AATCATATATTTGTAATATAGCAATTTGTCATATTTGAATTTAGTATTTAGACGG 1140
QY 1141 TTATCAGTCCAGCCAAATATGATTTGATTTAGTCCAAATGCAATTTGCTAGCTATCC 1200
DB 1141 TTATCAGTCCAGCCAAATATGATTTGATTTAGTCCAAATGCAATTTGCTAGCTATCC 1200
QY 1201 CTCTTGTCTCTAATGATTTATTCATATTTCTTATATATCCCTAATACAGAGCTACA 1260
DB 1201 CTCTTGTCTCTAATGATTTATTCATATTTCTTATATATCCCTAATACAGAGCTACA 1260
QY 1261 TTTATATTTGATTTCTAATGACAGGGAACCTTCATAGAGATTGATGATGAATTTGGT 1320
DB 1261 TTTATATTTGATTTCTAATGACAGGGAACCTTCATAGAGATTGATGATGAATTTGGT 1320
QY 1321 GGAACATCATTTGAACAGGAACCTTTAGCAATCATATCGATTTATCTACAAAGAAT 1380
DB 1321 GGAACATCATTTGAACAGGAACCTTTAGCAATCATATCGATTTATCTACAAAGAAT 1380
QY 1381 ACTTAGCGTAATGAGTTCACCTGTTGTAATGACTATGATTTGATCAAAATTTAGTTAAT 1440
DB 1381 ACTTAGCGTAATGAGTTCACCTGTTGTAATGACTATGATTTGATCAAAATTTAGTTAAT 1440
QY 1441 TTGTCGAATCATTTCTTTTGTGATTTGATTAAGCTTTTAACTTGACAGAAATGTTCTCT 1500
DB 1441 TTGTCGAATCATTTCTTTTGTGATTTGATTAAGCTTTTAACTTGACAGAAATGTTCTCT 1500
QY 1501 TGTGAATTAACAGAAATCTTGAATTCAAAGTATTTGATTTAGTGAAGAACAAAGAGAT 1560
DB 1501 TGTGAATTAACAGAAATCTTGAATTCAAAGTATTTGATTTAGTGAAGAACAAAGAGAT 1560
QY 1561 TCCTTGTTTTATGATTTAGTATTTGATTTGATGCAAGGAAGTACCTACGTACTACAAGAA 1620
DB 1561 TCCTTGTTTTATGATTTAGTATTTGATTTGATGCAAGGAAGTACCTACGTACTACAAGAA 1620
QY 1621 AAATTAACATGTACGTAACGTAATGATTCAGATGTAAGATTTTTCCTCAATTAATTTA 1680
DB 1621 AAATTAACATGTACGTAACGTAATGATTCAGATGTAAGATTTTTCCTCAATTAATTTA 1680
QY 1681 TACTCATGATAGATTTTTTTTTTTTGAATGTCAATTAATAAATGCTTCTTAATAATTTAA 1740
DB 1681 TACTCATGATAGATTTTTTTTTTTTGAATGTCAATTAATAAATGCTTCTTAATAATTTAA 1740
QY 1741 TTTTAATTAATTAAGAAATATATTTATGCAAAACATCATCAACATATCCAACT 1800
DB 1741 TTTTAATTAATTAAGAAATATATTTATGCAAAACATCATCAACATATCCAACT 1800
QY 1801 TCGAAATCTCTATAGTACAGAGTGAAGAAATTAATTTTACTAGTACAAACTCTCTA 1860
DB 1801 TCGAAATCTCTATAGTACAGAGTGAAGAAATTAATTTTACTAGTACAAACTCTCTA 1860
QY 1861 ATCATCATTTAATATGTTTACAAAACTAATTTAAACCCACGACTAAAATTTAACTAAAAT 1920

CC The invention relates to a genetic construct comprising senescence
CC specific promoter, preferably senescence associated gene (SAG)-12
CC promoter operably connected to a protein-coding DNA sequence not natively
CC connected to the promoter. The senescence associated promoters are useful
CC for the creation of transgenic plants with altered senescence
CC characteristics. Genetic constructs can be inserted into plants which
CC become effective only upon plant cells entering senescence. For example,
CC a gene encoding a biosynthetic enzyme under the control of a senescence-
CC specific promoter can be inserted into a plant, without having the
CC tissues of the plant exposed to the excess of cytokinin during pre-
CC senescence growth. Then at the onset of senescence, the senescence-
CC specific promoter activates cytokinin production to alter the progression
CC of senescence in the plant. The present sequence is a chimeric construct
CC comprising Arabidopsis thaliana SAG12 promoter, isopentenyl transferase
CC (IPT) gene and NOS-ter sequence. Note: This sequence is stated to be same
CC as that shown as SEQ ID NO:1 (AABD33336) in Column 15-20 of the
CC specification. However the sequences differ at several positions
XX

5Q Sequence 3183 BP; 1042 A; 528 C; 559 G; 1054 T; 0 U; 0 Other;

Query Match 99.8%; Score 3178.2; DB 6; Length 3183;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3180; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATATCTCTTTTATATCAACAATAAGTTGAGATATGTTGAGAAGAGACAACTATT 60
DB 1 GATATCTCTTTTATATCAACAATAAGTTGAGATATGTTGAGAAGAGACAACTATT 60
QY 61 CTGCTGGAGCACCAGAGTCTGTTTATATAGAAACCCGATGTTATTTTACACTGAGAC 120
DB 61 CTGCTGGAGCACCAGAGTCTGTTTATATAGAAACCCGATGTTATTTTACACTGAGAC 120
QY 121 AAAAAAGTAAATCGTTGATGTTTAAATTTAAATTAAGTTTCATCAAGTTTGAATAAA 180
DB 121 AAAAAAGTAAATCGTTGATGTTTAAATTTAAATTAAGTTTCATCAAGTTTGAATAAA 180
QY 181 AAATGATAGTTATCATAGCTAATAATAGCATGATTTCTAAATTTGTTTGGACACCCCTT 240
DB 181 AAATGATAGTTATCATAGCTAATAATAGCATGATTTCTAAATTTGTTTGGACACCCCTT 240
QY 241 TTTCTCTCTTTGGTGTCTTCTTAACATTAAGAAGACCATAACATGTAAGTCAAAAT 300
DB 241 TTTCTCTCTTTGGTGTCTTCTTAACATTAAGAAGACCATAACATGTAAGTCAAAAT 300
QY 301 AATTAAAAACAATATTTCCAGTTTATATACGAAACTGTGTTTAAATGAAACAGATT 360
DB 301 AATTAAAAACAATATTTCCAGTTTATATACGAAACTGTGTTTAAATGAAACAGATT 360
QY 361 GAATAGTTGATTAAGATTAGTAGATCAATCAATATATATGATGATGATATATAT 420
DB 361 GAATAGTTGATTAAGATTAGTAGATCAATCAATATATATGATGATGATATATAT 420
QY 421 ATGAAGTCAAGTTGTTATACAAGAAATGAAATGCTATTAAATACCGATCATGAAGTGT 480
DB 421 ATGAAGTCAAGTTGTTATACAAGAAATGAAATGCTATTAAATACCGATCATGAAGTGT 480
QY 481 AAAAAGTGCAGAAATGACATGAAGCGTTTGTCTTACCGGATCGAGTTATAGGTTT 540
DB 481 AAAAAGTGCAGAAATGACATGAAGCGTTTGTCTTACCGGATCGAGTTATAGGTTT 540
QY 541 GATCTCTCAAGAAATTTTGGGCCATATTAGTATATTTGGGCTTAAGCGTTTGCAAA 600
DB 541 GATCTCTCAAGAAATTTTGGGCCATATTAGTATATTTGGGCTTAAGCGTTTGCAAA 600
QY 601 GAGACGAGGAAAGATTGGGTCAAGTTAACAACACAGACACTCGATTTAGTTGTTA 660
DB 601 GAGACGAGGAAAGATTGGGTCAAGTTAACAACACAGACACTCGATTTAGTTGTTA 660
QY 661 CTTTGTAGCAAGTCAATTATTTGCGAGTAAAACTTGTTACACAACTGACAACTCGTA 720
DB 661 CTTTGTAGCAAGTCAATTATTTGCGAGTAAAACTTGTTACACAACTGACAACTCGTA 720
QY 721 TCGTTATTAGTTTGTACTGTGTACCTTTGTTAAGAAAAAGTGTATATAGTTAAATCAGT 780

DB 721 TCGTTATTAGTTTGTACTGTGTACCTTTGTTAAGAAAAAGTGTATATAGTTAAATCAGT 780
QY 781 TGTGTTCAAGAGTATGTGATTTAATTTGTGACTAGGCGGATTCCTTCAATCACA 840
DB 781 TGTGTTCAAGAGTATGTGATTTAATTTGTGACTAGGCGGATTCCTTCAATCACA 840
QY 841 TAACAAAGTTTATAGATTTTTTTTATATACATTTTTGCCACGCTTCGTAAGTTGGTA 900
DB 841 TAACAAAGTTTATAGATTTTTTTTATATACATTTTTGCCACGCTTCGTAAGTTGGTA 900
QY 901 TTACACCCGATTTTCCCTGTACAAAGATTCATATATTATTATTATATATCTCCAGT 960
DB 901 TTACACCCGATTTTCCCTGTACAAAGATTCATATATTATTATTATATATCTCCAGT 960
QY 961 GACAATTATAGTTTATTAACGTTTATTAACAATTATTAATTAATTAATTAATTAATTA 1020
DB 961 GACAATTATAGTTTATTAACGTTTATTAACAATTATTAATTAATTAATTAATTAATTA 1020
QY 1021 TATGCTTACTCTTCTTGTGTAGAAAACTAATATATCATATATATATATATATATATCT 1080
DB 1021 TATGCTTACTCTTCTTGTGTAGAAAACTAATATATCATATATATATATATATATATCT 1080
QY 1081 AATCATTTATTTTGTAAATATATGACGTTATTTGTCAATTTTGAATTTAGTATTTTGAACG 1140
DB 1081 AATCATTTATTTTGTAAATATATGACGTTATTTGTCAATTTTGAATTTAGTATTTTGAACG 1140
QY 1141 TTATCACTTCAGCCAAATATGATTTGGATTTAAGTCCAAATGCAATTTGTAAGTCC 1200
DB 1141 TTATCACTTCAGCCAAATATGATTTGGATTTAAGTCCAAATGCAATTTGTAAGTCC 1200
QY 1201 CTCTGTGCTCTAATGATTAATTTCAATATTTCTTATATATATATATATATATATATATAT 1260
DB 1201 CTCTGTGCTCTAATGATTAATTTCAATATTTCTTATATATATATATATATATATATATAT 1260
QY 1261 TTTATATTGTTATTTCTAATGACAGGAACTTTCAATAGATTCAGATAGTGAATTTGCT 1320
DB 1261 TTTATATTGTTATTTCTAATGACAGGAACTTTCAATAGATTCAGATAGTGAATTTGCT 1320
QY 1321 GGGAAACATCATTTGAACAGAGAACTTTAGCAAAATCATATGATTTATCTACAAAGAAAT 1380
DB 1321 GGGAAACATCATTTGAACAGAGAACTTTAGCAAAATCATATGATTTATCTACAAAGAAAT 1380
QY 1381 ACTTACCGTAAATGAAGTTCACTTGTGTGAATGACATGATTTGATCAAAATTAGTTAAT 1440
DB 1381 ACTTACCGTAAATGAAGTTCACTTGTGTGAATGACATGATTTGATCAAAATTAGTTAAT 1440
QY 1441 TTGTGCAATCATTTTCTTTTGTGATTTGATTAAGCTTTTAACTTGACAGAAATGTTCTCT 1500
DB 1441 TTGTGCAATCATTTTCTTTTGTGATTTGATTAAGCTTTTAACTTGACAGAAATGTTCTCT 1500
QY 1501 TGTGAATTAACAGAACTTTGGAATTCAAACTATTGATTTAGTGAAGAAAGAAAGAT 1560
DB 1501 TGTGAATTAACAGAACTTTGGAATTCAAACTATTGATTTAGTGAAGAAAGAAAGAT 1560
QY 1561 TCCCTGTTTATGTTAGTTAGTATTTGATGATGAAGAAAGTACCTACGTACTACAGAA 1620
DB 1561 TCCCTGTTTATGTTAGTTAGTATTTGATGATGAAGAAAGTACCTACGTACTACAGAA 1620
QY 1621 AAATAAACATGTACGTAAGTACGTAAGTACGTAAGTACGTAAGTACGTAAGTACGTAAGT 1680
DB 1621 AAATAAACATGTACGTAAGTACGTAAGTACGTAAGTACGTAAGTACGTAAGTACGTAAGT 1680
QY 1681 TACTCATGATAGATTTTTTTTTTTTGAAGTCAATTAAGAAATGCTTCTTAATATTTAA 1740
DB 1681 TACTCATGATAGATTTTTTTTTTTTGAAGTCAATTAAGAAATGCTTCTTAATATTTAA 1740
QY 1741 TTTTAAATTAATTAATTAAGAAATATATTAAGCAAAACATCATCAATATCCAACT 1800
DB 1741 TTTTAAATTAATTAATTAAGAAATATATTAAGCAAAACATCATCAATATCCAACT 1800
QY 1801 TCGAAATCTCTATAGTACACAGAGTACGAAATTAATTTTACTAGATACAAACTCTCTA 1860

Db 1801 TCGAAATCTCTAAGTACACAAGTAGAGAAAAATAATTTTACTAGATACAAACTTCCTA 1860
QY 1861 ATCATCATTTATAATGTTTACAAAACTAATTAACCCACTAAAAATTAACCTAAAAAT 1920
Db 1861 ATCATCATTTATAATGTTTACAAAACTAATTAACCCACTAAAAATTAACCTAAAAAT 1920
QY 1921 CCGAGCAAAAGTAGTGACAAACAAGACTTGATTTTCAGGTTGATGTAGAGCTAAATGCGCTACG 1980
Db 1921 CCGAGCAAAAGTAGTGACAAACAAGACTTGATTTTCAGGTTGATGTAGAGCTAAATGCGCTACG 1980
QY 1981 TATCAAAACATCAACGATCATTTAGTTATGTATGAATGAATGTAGTCAATTAACCTTAAC 2040
Db 1981 TATCAAAACATCAACGATCATTTAGTTATGTATGAATGAATGTAGTCAATTAACCTTAAC 2040
QY 2041 AAAAATGCTTTGATTTGATCAATCACTTCATGTGAACATTAAGCAATTACATCAACCTTA 2100
Db 2041 AAAAATGCTTTGATTTGATCAATCACTTCATGTGAACATTAAGCAATTACATCAACCTTA 2100
QY 2101 TTTTCACTATAAAACCCCACTCAGTACCCTTCTGAAGTAATCAAAATTAAGAGCAAAAGT 2160
Db 2101 TTTTCACTATAAAACCCCACTCAGTACCCTTCTGAAGTAATCAAAATTAAGAGCAAAAGT 2160
QY 2161 CATTTAATCTTCTTAATAAACCATGAGACCCCTGCATCTAATTTTCGGTCCAACTTGACAGGA 2220
Db 2161 CATTTAATCTTCTTAATAAACCATGAGACCCCTGCATCTAATTTTCGGTCCAACTTGACAGGA 2220
QY 2221 AAGACGACGACCGCGATAGCTCTTGCCAGACAGACAGGCTTCCAGTCTTCGCTTGAT 2280
Db 2221 AAGACGACGACCGCGATAGCTCTTGCCAGACAGACAGGCTTCCAGTCTTCGCTTGAT 2280
QY 2281 CGGCTCCAATCGTGTCTCAACTATCAACCGGAAGCGAGCAACCAAGTGAAGAACTG 2340
Db 2281 CGGCTCCAATCGTGTCTCAACTATCAACCGGAAGCGAGCAACCAAGTGAAGAACTG 2340
QY 2341 AAAGGAACGACGCGTCTCTACCTGATGATCGGCTCTGTTGAGAGGTATCATCGCAGCC 2400
Db 2341 AAAGGAACGACGCGTCTCTACCTGATGATCGGCTCTGTTGAGAGGTATCATCGCAGCC 2400
QY 2401 AAGCAAGCTCATCATAGGCTGATCGAGAGGTGTATATCATGAGGCCAACGCGGGCTT 2460
Db 2401 AAGCAAGCTCATCATAGGCTGATCGAGAGGTGTATATCATGAGGCCAACGCGGGCTT 2460
QY 2461 ATTCTTGAGGGAGGATCCACCTCGTGTCTCAACTGCATGCGCGGCAACAGCTATTGGAGT 2520
Db 2461 ATTCTTGAGGGAGGATCCACCTCGTGTCTCAACTGCATGCGCGGCAACAGCTATTGGAGT 2520
QY 2521 GCAGATTTTCGTTGGCATATTATTCGCCACAAGTTACCCGACCAAGAGACCTTCATGAAA 2580
Db 2521 GCAGATTTTCGTTGGCATATTATTCGCCACAAGTTACCCGACCAAGAGACCTTCATGAAA 2580
QY 2581 GCGGCCAAGGCCAGAGTTAAGCAGATGTGCAACCCGCTGCAGGCCATTCTATTATTCAA 2640
Db 2581 GCGGCCAAGGCCAGAGTTAAGCAGATGTGCAACCCGCTGCAGGCCATTCTATTATTCAA 2640
QY 2641 GAGTGTGTTATCTTTGGAATGAACCTCGGCTGAGGCCCATTTGAAAGAGATCGATGGA 2700
Db 2641 GAGTGTGTTATCTTTGGAATGAACCTCGGCTGAGGCCCATTTGAAAGAGATCGATGGA 2700
QY 2701 TATCGATATGCCATGTTGTTTGTAGCCAGAACCCAGATCAACGCAAGTATGCTATTGCAG 2760
Db 2701 TATCGATATGCCATGTTGTTTGTAGCCAGAACCCAGATCAACGCAAGTATGCTATTGCAG 2760
QY 2761 CTGACGCAAAATATGGAAGGTAAGTGAATGAGGATCGCTCAGAGATATTTCATCCAT 2820
Db 2761 CTGACGCAAAATATGGAAGGTAAGTGAATGAGGATCGCTCAGAGATATTTCATCCAT 2820
QY 2821 GCGCGCCAAACAGGAACAAGAAATTCGCCCAAGTTAACGCAAGCCGCTTTCGACGGAATCGAA 2880
Db 2821 GCGCGCCAAACAGGAACAAGAAATTCGCCCAAGTTAACGCAAGCCGCTTTCGACGGAATCGAA 2880
QY 2881 GGTGATCCGTTGGAATGTATTAGGTTACGCCAGCCCTGAGCTCGATCGTTCAACAATTT 2940
Db 2881 GGTGATCCGTTGGAATGTATTAGGTTACGCCAGCCCTGAGCTCGATCGTTCAACAATTT 2940

QY 2941 GGCAATAAGTTTCTTAAGATTTGAATCCGTGCGGCTTGCGATGATATCATATPAT 3000
Db 2941 GGCAATAAGTTTCTTAAGATTTGAATCCGTGCGGCTTGCGATGATATCATATPAT 3000
QY 3001 TTCTGTGAATTAAGTTAAGCATGTAAATTAACATGTAAATGATGACGTTATTATGA 3060
Db 3001 TTCTGTGAATTAAGTTAAGCATGTAAATTAACATGTAAATGATGACGTTATTATGA 3060
QY 3061 GATGGGTTTATGATTTAGAGTCCCGCAATTATACATTTAATACGCGATGAAAAACAAA 3120
Db 3061 GATGGGTTTATGATTTAGAGTCCCGCAATTATACATTTAATACGCGATGAAAAACAAA 3120
QY 3121 TATGCGCGCAACTGGGATTAATTATCGCGCGGCTGTCATCTATGTTACTAGATCGAA 3180
Db 3121 TATGCGCGCAACTGGGATTAATTATCGCGCGGCTGTCATCTATGTTACTAGATCGAA 3180
QY 3181 TTC 3183
Db 3181 TTC 3183

RESULT 3
AAD33336
ID AAD33336 standard; DNA; 3182 BP.
XX
AC AAD33336;
XX
DT 01-JUL-2002 (first entry)
XX
DE A. thaliana SAG12 promoter/IPT/NOS-ter construct (alternative version).
XX
KM Senescence associated gene; SAG-12; transgenic plant; transgenic;
KM senescence-specific promoter; senescence characteristic; chimeric; IPT;
KM isopenentenyl transferase; NOS-ter; ds.
XX
OS Arabidopsis thaliana.
OS unidentified.
OS Chimeric.
FN US6359197-B1.
XX
PD 19-MAR-2002.
XX
PF 17-NOV-1997; 97US-00971395.
PR 29-MAR-1995; 95US-00413135.
XX
PA (WISC) WISCONSIN ALUMNI RES FOUND.
PI Amasino RM, Gan S, Noh Y;
XX
DR WPI; 2002-291012/33.
XX
PT Novel senescence associated promoter sequence connected to a protein-
PT coding DNA sequence useful for the creation of transgenic plants with
XX altered senescence characteristics.
PS Claim 1; Col 15-20; 21pp; English.
XX
XX The invention relates to a genetic construct comprising senescence
CC specific promoter, preferably senescence associated gene (SAG)-12
CC promoter operably connected to a protein-coding DNA sequence not nativel
CC connected to the promoter. The senescence associated promoters are useful
CC for the creation of transgenic plants with altered senescence
CC characteristics. Genetic constructs can be inserted into plants which
CC become effective only upon plant cells entering senescence. For example,
CC a gene encoding a biosynthetic enzyme under the control of a senescence-
CC specific promoter can be inserted into a plant, without having the
CC tissues of the plant exposed to the excess of cytokinin during pre-
CC senescence growth. Then at the onset of senescence, the senescence-
CC specific promoter activates cytokinin production to alter the progression
CC of senescence in the plant. The present sequence is an alternative

Db 1981 TATCAACATCAACGATCATTTAGTTATGTATGAATGAATGTAGTCATTACTTGTAAAC 2040
QY 2041 AAAAATGCTTTGATTTGGATCAATCACTTCATGTGAACATTAGCAATTACATCAACCTTA 2100
Db 2041 AAAAATGCTTTGATTTGGATCAATCACTTCATGTGAACATTAGCAATTACATCAACCTTA 2100
QY 2101 TTTTCACTATAAAACCCCATCTCAGTACCCCTTCTGAAGTAATCAAAATTAAGAGCAAAAGT 2160
Db 2101 TTTTCACTATAAAACCCCATCTCAGTACCCCTTCTGAAGTAATCAAAATTAAGAGCAAAAGT 2160
QY 2161 CATTTAACTTTCCTAAAAACCATGAGACCCCTGCATCTAATTTTGGTCCAACTTGACAGAGA 2220
Db 2161 CATTTAACTTTCCTAAAAACCATGAGACCCCTGCATCTAATTTTGGTCCAACTTGACAGAGA 2219
QY 2221 AAGACGAGACCCGCGATAGCTCTTGCCACAGACAGAGGGCTTCCAGTCTTTCGCTTGAT 2280
Db 2220 AAGACGAGACCCGCGATAGCTCTTGCCACAGACAGAGGGCTTCCAGTCTTTCGCTTGAT 2279
QY 2281 CGGTCGAATCGTGTCTCTCAACTATCAACCGGAAGCGGACGACCAAGTGAAGAAGT 2340
Db 2280 CGGTCGAATCGTGTCTCTCAACTATCAACCGGAAGCGGACGACCAAGTGAAGAAGT 2339
QY 2341 AAAGGACGACCGCTCTCTACCTTGATATCGGCTCTGTGAGGGTATCATCGCAGCC 2400
Db 2340 AAAGGACGACCGCTCTCTACCTTGATATCGGCTCTGTGAGGGTATCATCGCAGCC 2399
QY 2401 AAGCAAGCTCATCATAGGCTGATCGAGGAGGTATATCATCATGAGGCCAAAGGGGGCTT 2460
Db 2400 AAGCAAGCTCATCATAGGCTGATCGAGGAGGTATATCATCATGAGGCCAAAGGGGGCTT 2459
QY 2461 ATCTTTGAGGAGGATCCACCTCGTTGCTCAACTGCATGGCGGCAACAGCTATTGGAGT 2520
Db 2460 ATCTTTGAGGAGGATCCACCTCGTTGCTCAACTGCATGGCGGCAACAGCTATTGGAGT 2519
QY 2521 GCAGATTTTCGTTGGCATATTATTGCGCCAGAGTTACCCGACCAAGAGACCTTCATGAAA 2580
Db 2520 GCAGATTTTCGTTGGCATATTATTGCGCCAGAGTTACCCGACCAAGAGACCTTCATGAAA 2579
QY 2581 GCGGCCAAGGCCAGATTAAAGCAGATGTGCACCCCGCTGCAGGCCATTTCTATTCAA 2640
Db 2580 GCGGCCAAGGCCAGATTAAAGCAGATGTGCACCCCGCTGCAGGCCATTTCTATTCAA 2639
QY 2641 GAGTTGTTTATCTTTGGAATGAACCTCGGCTGAGGCCCATTTCTGAAGAAGATCGATGGA 2700
Db 2640 GAGTTGTTTATCTTTGGAATGAACCTCGGCTGAGGCCCATTTCTGAAGAAGATCGATGGA 2699
QY 2701 TATCGATATGCCATGTGTTGTTGCTAGCCAGAACAGATCAAGGAGATATGCTATTGCGAG 2760
Db 2700 TATCGATATGCCATGTGTTGTTGCTAGCCAGAACAGATCAAGGAGATATGCTATTGCGAG 2759
QY 2761 CTGACGCAATATGGAAGTTAAGTTGATTAATGGATCGCTCAGAGATTTTCATCCAT 2820
Db 2760 CTGACGCAATATGGAAGTTAAGTTGATTAATGGATCGCTCAGAGATTTTCATCCAT 2819
QY 2821 GCGCGCCACAGAGAACAGAAATCCCCCAAGTTAAAGCAGAGCCGCTTCGACGGAGTTGAA 2880
Db 2820 GCGCGCCACAGAGAACAGAAATCCCCCAAGTTAAAGCAGAGCCGCTTCGACGGAGTTGAA 2879
QY 2881 GGTTCATCCGTTCCGAATGTATTAAGTTACGCCAGCCCTGAGCTCGATCGTCAACATTT 2940
Db 2880 GGTTCATCCGTTCCGAATGTATTAAGTTACGCCAGCCCTGAGCTCGATCGTCAACATTT 2939
QY 2941 GCGAATAAAGTTCTTAAGATGAATCCTGTTGCCGCTTTCGATGATTAATCAATAAT 3000
Db 2940 GCGAATAAAGTTCTTAAGATGAATCCTGTTGCCGCTTTCGATGATTAATCAATAAT 2999
QY 3001 TTTCTGTGAATTACGTTAAGCATGTAAATTAATTAACATGTAAATGATGAGCTTAATTATGA 3060
Db 3000 TTTCTGTGAATTACGTTAAGCATGTAAATTAATTAACATGTAAATGATGAGCTTAATTATGA 3059
QY 3061 GATGGTTTTTATGATTAGATCCCGCAATTATACATTTAATAACGCGATAGAAAACAAA 3120
Db 3060 GATGGTTTTTATGATTAGATCCCGCAATTATACATTTAATAACGCGATAGAAAACAAA 3119

QY 3121 TATGGCGCGCAAACTGGGATAAATTATCGCGCGGTGTCTATGTATTACTAGATCGAA 3180
Db 3120 TATGGCGCGCAAACTGGGATAAATTATCGCGCGGTGTCTATGTATTACTAGATCGAA 3179
QY 3181 TTC 3183
Db 3180 TTC 3182

RESULT 4
AAV69757
ID AAV69757 standard; DNA; 745 BP.
XX
AC AAV69757;
XX
DT 01-MAR-1999 (first entry)
XX
DE Isopenentenyl transferase ipt gene.
XX
KW Isopenentenyl transferase; ipt gene; cytokinin; transgenic plant;
KW seedless fruit; tomato; watermelon; cucumber; ds.
XX
OS Agrobacterium tumefaciens.
XX
FH Key Location/Qualifiers
FT CDS 3..725
FT /*tag= a
XX
PN W09849888-A1.
XX
PD 12-NOV-1998.
XX
PF 06-MAY-1998; 98WO-US009013.
XX
PR 06-MAY-1997; 97US-0045725P.
XX
PA (UNIV) UNIV KANSAS STATE RES FOUND.
XX
PI L1 Y;
XX
DR WPI; 1999-034673/03.
DR P-PSDB; AAW81575.
XX
PT A new construct to express phytohormones in developing fruit - useful
PT for, e.g. producing substantially seedless fruit from transgenic plants.
XX
PS Example 1; Page 31-33; 49pp; English.
XX
CC This is the nucleotide sequence of the Agrobacterium tumefaciens ipt gene
CC that codes for isopenentenyl transferase (see AAW81575), an enzyme of the
CC cytokinin biosynthetic pathway. A claimed DNA construct comprises either
CC an isopenentenyl transferase or a tryptophan oxygenase (see AAW81574)
CC encoding sequence, operably linked to an ovary or developing fruit-
CC specific plant-expressible promoter (see AAV69755 and AAV69759). The
CC construct is used to stably integrate enzymes involved in cytokinin or
CC auxin biosynthesis into the plant genome to achieve a transgenic plant
CC (preferably tomato, cucumber or watermelon) producing seedless fruit in
CC the absence of pollination
XX
SQ Sequence 745 BP; 193 A; 185 C; 192 G; 175 T; 0 U; 0 Other;

Query Match 23.1%; Score 734.8; DB 2; Length 745;
Best local Similarity 99.7%; Pred. No. 2.4e-114;
Matches 736; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2187 CCTGCATCTAATTTTCGTTCCAACTTGACACAGAAAGACGACGCGGATAGCTCTTGC 2246
Db 8 CTTGCACTAATTTTCGTTCCAACTTGACACAGAAAGACGACGCGGATAGCTCTTGC 67
QY 2247 CCAGCAGACAGGGCTTCCAGTCTTTCGCTTGATCGGCTCCATCGTCTCAACTATC 2306
Db 68 CCAGCAGACAGGGCTTCCAGTCTTTCGCTTGATCGGCTCCATCGTCTCAACTATC 127

QY 2307 AACCGGAAGCGGACGACCAACAGTGAAGAAGTGAAGAAGGAAAGGCGGCTCTCTACCTTGA 2366
DB 128 AACCGGAAGCGGACGACCAACAGTGAAGAAGTGAAGAAGGAAAGGCGGCTCTCTACCTTGA 187
QY 2367 TGAATCGGCTCTGTGTGAGGGTATCATCGACGCCAAGCAAGCTCATCATAGGCTGATCGA 2426
DB 188 TGAATCGGCTCTGTGTGAGGGTATCATCGACGCCAAGCAAGCTCATCATAGGCTGATCGA 247
QY 2427 GGAGGTGATATATCATGAGGCCAAGCGGGGCTTATCTTGAGGAGAGATCCACCTCGTT 2486
DB 248 GGAGGTGATATATCATGAGGCCAAGCGGGGCTTATCTTGAGGAGAGATCCACCTCGTT 307
QY 2487 GCTCAATGTCATGGCGCGAAGACAGCTATTTGAGTGCAGATTTTCGTTGGCATATTTTCG 2546
DB 308 GCTCAATGTCATGGCGCGAAGACAGCTATTTGAGTGCAGATTTTCGTTGGCATATTTTCG 367
QY 2547 CCACAAAGTACCCGACCAAGAGACCTTCATGAAAGCGGCCAAGGCCAGAGTTAAGCAGAT 2606
DB 368 CCACAAAGTACCCGACCAAGAGACCTTCATGAAAGCGGCCAAGGCCAGAGTTAAGCAGAT 427
QY 2607 GTTGACCCCGCTGCAGGCCATTCATTAATTCAGAGTTGGTTATCTTTGGAATGAACC 2666
DB 428 GTTGACCCCGCTGCAGGCCATTCATTAATTCAGAGTTGGTTATCTTTGGAATGAACC 487
QY 2667 TCGGCTGAGGCCCATTTCTGAAGAAGATCGATGATATCGATATGCCATGTTGTTGCTAG 2726
DB 488 TCGGCTGAGGCCCATTTCTGAAGAAGATCGATGATATCGATATGCCATGTTGTTGCTAG 547
QY 2727 CCAGAACCAATCAACGCGACATATGCTATTCAGCTTGACGCAATATGGAAGTAAGTT 2786
DB 548 CCAGAACCAATCAACGCGACATATGCTATTCAGCTTGACGCAATATGGAAGTAAGTT 607
QY 2787 GATTATGGGATCGCTCAGAGATTTTCATCCATGCGCGCCCAACAGAAACAGAAATTTCCC 2846
DB 608 GATTATGGGATCGCTCAGAGATTTTCATCCATGCGCGCCCAACAGAAACAGAAATTTCCC 667
QY 2847 CCAAGTTAAGCAGCGGCTTTGACGGATTCGAAGTCAATCCGTTCCGAATGTATTAGT 2906
DB 668 CCAAGTTAAGCAGCGGCTTTGACGGATTCGAAGTCAATCCGTTCCGAATGTATTAGT 727
QY 2907 TACGCCAGCCCTGAGCTC 2924
DB 728 TACGCCAGCCCTGAGCTC 745
RESULT 5
ID ABK12492 standard; DNA; 1988 BP.
XX
AC ABK12492;
XX
DT 18-JUN-2002 (first entry)
XX
DE Agrobacterium tumefaciens isopentenyl transferase (ipt) gene.
XX
KW Isopentenyl transferase; ipt; myb32; promoter; transgenic; plant;
KW senescence; cytokinin biosynthesis; shelf life; fruit; flower; leaf;
KW tuber; horticulture; carbon fixation; biomass; forage crop;
KW seed production; root growth; shoot growth; root formation;
KW apical dominance; gene; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO200220772-A1.
XX
PD 14-MAR-2002.
XX
PF 30-AUG-2001; 2001WO-AU001092.
XX
PR 06-SEP-2000; 2000AU-00009946.
XX
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.

PA (UYLT-) UNIV LA TROBE.
XX Spangenberg G, Lin YH, Parish RW, Li SF, Heazlewood J;
PI Pallaighy CK;
PI
XX
DR WPI; 2002-304382/34.
XX
PT Manipulating plant senescence, useful e.g. for increasing shelf life of
PT fruit, comprises expressing gene involved in cytokine synthesis under
PT control of myb gene promoter.
XX
PS Claim 7; Fig 2; 27pp; English.

CC The invention describes a method of manipulating senescence in a plant
CC comprising introducing a genetic construct that includes a myb gene
CC promoter linked to a gene encoding an enzyme involved in biosynthesis of
CC a cytokinin, where both the promoter and the gene may be used as
CC functionally active fragments or variants. Manipulation (specifically,
CC delay) of senescence is used to increase shelf life of fruits, flowers,
CC leaves and tubers in horticultural crops, improve carbon fixation (and thus
CC perishability of horticultural crops, improve carbon fixation (and thus
CC yield, including biomass in forage crops) and increase seed production.
CC Use of the myb gene promoter (unlike other promoters used for
CC overexpression of the cytokinin biosynthesis gene) does not cause
CC retarded root and shoot growth, failure of root formation, reduced apical
CC dominance and reduced leaf area. This sequence represents the
CC Agrobacterium tumefaciens isopentenyl transferase (ipt) gene, the product
CC of which is involved in cytokinin biosynthesis
XX

SQ Sequence 1988 BP; 593 A; 386 C; 406 G; 603 T; 0 U; 0 Other;

Query Match 23.0%; Score 733.4; DB 6; Length 1988;
Best Local Similarity 96.0%; Pred. No. 4.3e-114;
Matches 752; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 2139 TAAATCAATTAAGCAAAAGTCAATTTAATTCTTCTTAAACCAATGGAACCTGCATCTAAT 2198
DB 647 TAAATCAAAATCAAGTTTGTATTCATATCAATGCTGCAAAAACCTTAATGGAACCTGCATCTAAT 706
QY 2199 TTTGCTCCAACTTGACACAGAAAGACGACGCGGATAGCTCTTGCCACAGACAGAG 2258
DB 707 TTTGCTCCAACTTGACACAGAAAGACGACGCGGATAGCTCTTGCCACAGACAGAG 766
QY 2259 GCTTCAGTCTCTTTCGCTTGATCGGCTCCATCGTGTCTCTCAATCAATCAACCGGAACGG 2318
DB 767 GCTTCAGTCTCTTTCGCTTGATCGGCTCCATCGTGTCTCTCAATCAATCAACCGGAACGG 826
QY 2319 ACGACCAACAGTGAAGAACTGAAGAAAGACGCGCTCTCTACCTTGATGATCGGCTCT 2378
DB 827 ACGACCAACAGTGAAGAACTGAAGAAAGACGCGCTCTCTACCTTGATGATCGGCTCT 886
QY 2379 GGTGAGGGTATCATCGACGCCAAGCAAGCTCATATAGGCTGATCGAGAGGTATATA 2438
DB 887 GGTGAGGGTATCATCGACGCCAAGCAAGCTCATATAGGCTGATCGAGAGGTATATA 946
QY 2439 TCATGAGGCCAAGCGGGGCTTATTTTGAGGGAGATCCACCTCGTTGCTCAACTGCAT 2498
DB 947 TCATGAGGCCAAGCGGGGCTTATTTTGAGGGAGATCCACCTCGTTGCTCAACTGCAT 1006
QY 2499 GCGCGAAACAGCTATTGAGTGCAGATTTTCGTTGCGATATTATTCGCCACAAGTTACC 2558
DB 1007 GCGCGAAACAGCTATTGAGTGCAGATTTTCGTTGCGATATTATTCGCCACAAGTTACC 1066
QY 2559 CGACCAAGAGACCTTCATGAAGCGGCCAAGGCCAGAGTTAAGCAGATGTTGACACCCCGC 2618
DB 1067 CGACCAAGAGACCTTCATGAAGCGGCCAAGGCCAGAGTTAAGCAGATGTTGACACCCCGC 1126
QY 2619 TGCAGGCCATTTATTAATCAAGAGTTGGTTATCTTTGGAATGAACCTCGGCTGAGGCC 2678
DB 1127 TGCAGGCCATTTATTAATCAAGAGTTGGTTATCTTTGGAATGAACCTCGGCTGAGGCC 1186
QY 2679 CATTTGAAGAAGATCGATGATATCGATATGCCATGTTGTTGCTAGCCAGAACAGAT 2738

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Db 1187 CATTCTGAAGAGATCGATGATATCGATATGCCATGTGTTTGCTAGCCAGAACAGAT 1246
QY 2739 CACGGCAGATATGCTATTGACGCTTGACCAATATGGAAGGTAAGTTGATTAATGGAT 2798
Db 1247 CACGGCAGATATGCTATTGACGCTTGACCAATATGGAAGGTAAGTTGATTAATGGAT 1306
QY 2799 CGCTCAGAGATATTTCATCCATGCGGCCAACAGGAACAGAAATTCCTCCCAAGTTAACGC 2858
Db 1307 CGCTCAGAGATATTTCATCCATGCGGCCAACAGGAACAGAAATTCCTCCCAAGTTAACGC 1366
QY 2859 AGCCGCTTTCGACGGAATTCGAAAGTCAATCCGTTGGAATGATTAAGTTACGCCAGCCCT 2918
Db 1367 AGCCGCTTTCGACGGAATTCGAAAGTCAATCCGTTGGAATGATTAAGTTACGCCAGCCCT 1426
QY 2919 GAG 2921
Db 1427 GCG 1429

RESULT 6
AAN50182
ID AAN50182 standard; DNA; 24596 BP.
AC AAN50182;
XX
XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 17-OCT-1991 (first entry)
XX
DE Complete nucleotide sequence of the T-DNA region of the octopine Ti
DE plasmid pTi15955.
XX
XX Plant vector; transformation-inducing principle (TiP) gene;
KM octopine Ti plasmid; ss.
KM
XX Agrobacterium tumefaciens; ATCC 15955.
OS
XX
XX EP145338-A.
PN
XX 19-JUN-1985.
PD
XX 16-NOV-1984; 84EP-00307969.
PF
XX 18-NOV-1983; 83US-00553786.
PR
XX
XX (AGRK ) AGRIGENETICS RES ASSOC LTD.
PA (LUBR ) LUBRIZOL GENETICS INC.
XX
PI Barker RF, Kemp JD;
PI
XX WPI; 1985-148223/25.
DR
XX
XX New DNA vectors contg. T-DNA sequence of octopine Ti plasmid - for
PT expression in plant cells to confer desirable properties to plants and
PT their cells.
PT
XX
PS Claim 28; Fig 1; 87pp; English.
XX
XX The inventors claim a vector contg. a transformation-inducing principle
CC (TiP) gene from Ti plasmid pTi15955. The sequence of the T-DNA of the
CC octopine-type Ti plasmid has fourteen open reading frames bounded by
CC eukaryotic promoters, ribosome binding sites, and polyadenylation sites.
CC With the vectors, expression of structural foreign genes in plant cells
CC is promoted. The gene esp. encodes an insecticidal toxin identical to or
CC derived from the crystal protein of Bacillus thuringiensis. (Updated on
CC 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise
CC OS field)
XX
XX Sequence 24596 BP; 6534 A; 5510 C; 5793 G; 6759 T; 0 U; 0 Other;
SQ
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Query Match 23.0%; Score 733.4; DB 1; Length 24596;
Best Local Similarity 96.0%; Pred. No. 4.9e-114;
Matches 752; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
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QY 2139 TAATCAATTAGAGCAAAAGTCATTTAACCTTTCCTAAACCATGGAACCTGCATCTAAT 2198
Db 8728 TAATATAAAATCAGTTTGTAATTCAATATACTGCAAAAATACTATGACCTGCATCTAAT 8787
QY 2199 TTTCGGTCCAACTTGACAGAGAAAGACGACGACCGCGGATAGCTCTTGCCAGCAGACAGG 2258
Db 8788 TTTCGGTCCAACTTGACAGAGAAAGACGACGACCGCGGATAGCTCTTGCCAGCAGACAGG 8847
QY 2259 GCTTCCAGTCCCTTTCGCTTGATCGGGTCCAAATCGTGTCTCAACTATCAACCGGAAGCGG 2318
Db 8848 GCTTCCAGTCCCTTTCGCTTGATCGGGTCCAAATCGTGTCTCAACTATCAACCGGAAGCGG 8907
QY 2319 ACACCAACAGTGAAGAACTGAAGAAAGAACGACGCGTCTTAACCTTGATGATCGGCTCT 2378
Db 8908 ACACCAACAGTGAAGAACTGAAGAAAGAACGACGCGTCTTAACCTTGATGATCGGCTCT 8967
QY 2379 GGTGAGGGTATCATCGCAGCCAAAGCAAGCTCATATAGCTGATCGAGAGGTATATAA 2438
Db 8968 GGTGAGGGTATCATCGCAGCCAAAGCAAGCTCATATAGCTGATCGAGAGGTATATAA 9027
QY 2439 TCATGAGGCCAACGCGGGCTTATTCTTGAGGAGAGATCCACCTCGTGTCTCAACTGCAT 2498
Db 9028 TCATGAGGCCAACGCGGGCTTATTCTTGAGGAGAGATCCACCTCGTGTCTCAACTGCAT 9087
QY 2499 GGCGGCAACAGCTATTGAGTGAGATTTTCTGTTGGCATATATTGCGCACAAAGTTACC 2558
Db 9088 GGCGGCAACAGCTATTGAGTGAGATTTTCTGTTGGCATATATTGCGCACAAAGTTACC 9147
QY 2559 CGACCAAGAGACCTTCATGAAGCGGCCAAGGCCAGAGTTAAGCAGATGTGCACCCCGC 2618
Db 9148 CGACCAAGAGACCTTCATGAAGCGGCCAAGGCCAGAGTTAAGCAGATGTGCACCCCGC 9207
QY 2619 TGCAGGCCATTCTATTATTCAGAGTTGGTTTATCTTGGAAAGAACTCGGCTGAGGCC 2678
Db 9208 TGCAGGCCATTCTATTATTCAGAGTTGGTTTATCTTGGAAAGAACTCGGCTGAGGCC 9267
QY 2679 CATTCTGAAGAGATCGATGGATATTCGATATGCCATGTTGTTGCTAGCCAGAACAGAT 2738
Db 9268 CATTCTGAAGAGATCGATGGATATTCGATATGCCATGTTGTTGCTAGCCAGAACAGAT 9327
QY 2739 CACGGCAGATATGCTATTGACGCTTGACGCAATATGGAAGGTAAGTTAATGGAT 2798
Db 9328 CACGGCAGATATGCTATTGACGCTTGACGCAATATGGAAGGTAAGTTAATGGAT 9387
QY 2799 CGCTCAGAGATATTTCATCCATGCGGCCAACAGGAACAGAAATTCCTCCCAAGTTAACGC 2858
Db 9388 CGCTCAGAGATATTTCATCCATGCGGCCAACAGGAACAGAAATTCCTCCCAAGTTAACGC 9447
QY 2859 AGCCGCTTTCGACGGAATTCGAAAGTCAATCCGTTGGAATGATTAAGTTACGCCAGCCCT 2918
Db 9448 AGCCGCTTTCGACGGAATTCGAAAGTCAATCCGTTGGAATGATTAAGTTACGCCAGCCCT 9507
QY 2919 GAG 2921
Db 9508 GCG 9510
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RESULT 7
AAN50226
ID AAN50226 standard; DNA; 24593 BP.
AC AAN50226;
XX
XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-OCT-1991 (first entry)
XX
DE Sequence of opine synthase gene.
XX
XX Plant vector; Ti plasmid; T-DNA; ss.
KM
XX Agrobacterium tumefaciens; Ti plasmid.
OS
```

XX
PN EPI40556-A.
XX
PD 08-MAY-1985.
XX
PF 12-SEP-1984; 84EP-00306233.
XX
PR 14-SEP-1983; 83US-00532280.
XX
PA (AGRK) AGRIGENETICS RES ASSOC LTD.
PA (LUBR) LUBRIZOL GENETICS INC.
XX
PI Dahl GA, Sutton DW, Barker RF;
XX
DR WPI; 1985-112088/19.
XX
PT Plasmid contg. opine synthase gene for selection - and foreign DNA,
PT useful as vector for transforming plant cells.
XX
PS Disclosure; Page 212-217; 69pp; Japanese.
XX
CC Plant cells (and protoplasts) and plasmids contg. the DNA fragment which
CC includes an opine synthase gene plus a gene for antibiotic resistance are
CC claimed. These plasmids provide max. efficiency for transfer of foreign
CC genes and can be amplified in the plant genome. They do not contain genes
CC specifying tumour formation and will not spread antibiotic resistance
CC throughout the plant population. (Updated on 25-MAR-2003 to correct PF
CC field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-
CC 2003 to standardise OS field)
XX
SQ Sequence 24593 BP; 6554 A; 5493 C; 5787 G; 6759 T; 0 U; 0 Other;

Query Match 22.9%; Score 730.2; DB 1; Length 24593;
Best Local Similarity 95.8%; Pred. No. 1.7e-113;
Matches 750; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 2139 TAATCAATTAGAGCAAAAGTCATTACTTCTTAACCATGAGACCTGCATCTAAT 2198
DB 8728 TAATATAAAATCAGTTTGTATTCATATATCTGCAAAAACCTATGAGACTGCATCTAAT 8787
QY 2199 TTTCGGTCCAACCTTGCAAGAAAGACGACGACCGCGATAGCTCTTGCCCAAGACAGG 2258
DB 8788 TTTCGGTCCAACCTTGCAAGAAAGACGACGACCGCGATAGCTCTTGCCCAAGACAGG 8847
QY 2259 GCTTCAGTCCCTTTCGCTTGATCGGGTCCAATCGTCTCTCACTATCAACCGGAAGCGG 2318
DB 8848 GCTTCAGTCCCTTTCGCTTGATCGGGTCCAATCGTCTCTCACTATCAACCGGAAGCGG 8907
QY 2319 ACGACCAACAGTGAAGAACTGAAAGGAACGACGCGTCTCTACCTTGATGATCGGCTCT 2378
DB 8908 ACGACCAACAGTGAAGAACTGAAAGGAACGACGCGTCTCTACCTTGATGATCGGCTCT 8967
QY 2379 GGTGAGGGTATCATCGAGCCCAAGCTCATATAGGCTGATCGAGGAGGTATATA 2438
DB 8968 GGTGAGGGTATCATCGAGCCCAAGCTCATATAGGCTGATCGAGGAGGTATATA 9027
QY 2439 TCATGAGGCCCAACGGCGGCTTATTTTGAGGAGGATCCACCTCGTTGCTCAACTGCAT 2498
DB 9028 TCATGAGGCCCAACGGCGGCTTATTTTGAGGAGGATCCACCTCGTTGCTCAACTGCAT 9087
QY 2499 GGGCGGAAACAGCTATGTGAGTGCAGATTTTCGTTGGCATATTAATTCGCCACAAGTTACC 2558
DB 9088 GGGCGGAAACAGCTATGTGAGTGCAGATTTTCGTTGGCATATTAATTCGCCACAAGTTACC 9147
QY 2559 CGACCAAGAGACCTTCATGAAGCGGCCCAAGGCCAGAGTTAAGCAGATGTGCAACCCCGC 2618
DB 9148 CGACCAAGAGACCTTCATGAAGCGGCCCAAGGCCAGAGTTAAGCAGATGTGCAACCCCGC 9207
QY 2619 TGCAGGCCATCTATTATTCAAGAGTTGTTTATCTTTGGAATGAACCTCGGCTGAGGCC 2678
DB 9208 TGCAGGCCATCTATTATTCAAGAGTTGTTTATCTTTGGAATGAACCTCGGCTGAGGCC 9267
QY 2679 CATCTGAAGAAGATCGATGATATGATGATGATGATGATGATGATGATGATGATGATGAT 2738

DB 9268 CATTCTGAAGAGATCGATGATATGCATATGCCATGTTGTTGCTAGCCAGAACAGAT 9327
QY 2739 CACGGCAGATATGCTATTTCAGCTTGACGCAATATGGAAGGTAAGTTGATTAATGGAT 2798
DB 9328 CACGGCAGATATGCTATTTCAGCTTGACGCAATATGGAAGGTAAGTTGATTAATGGAT 9387
QY 2799 CGCTCAGAGATATTCATCCATGCGCGCCCAACAGAACAGAAATTCGCCAAGTTAAAGC 2858
DB 9388 CGCTCAGAGATATTCATCCATGCGCGCCCAACAGAACAGAAATTCGCCAAGTTAAAGC 9447
QY 2859 AGCCGCTTTCGACCGGATTCGAAGGTCATCCGTTCCGAATGATATTAGGTTACGCCAGCCT 2918
DB 9448 AGCCGCTTTCGACCGGATTCGAAGGTCATCCGTTCCGAATGATATTAGGTTACGCCAGCCT 9507
QY 2919 GAG 2921
DB 9508 GCG 9510

RESULT 8

AAD00619
ID AAD00619 standard; DNA; 723 BP.
XX
AC AAD00619;
XX
DT 29-AUG-2000 (first entry)
XX
DE Agrobacterium tumefaciens T-DNA gene, ipt.
XX
KW iaam; iaah; ipt; T-DNA; transferred DNA; gall-disease resistance; BR;
KW bacterial resistance construct; untranslatable RNA; tumour; oncogene;
KW cytokinin; plant growth hormone; ds.
XX
OS Agrobacterium tumefaciens.
XX
PN WO200026346-A1.
XX
PD 11-MAY-2000.
XX
PF 04-NOV-1999; 99WO-US026100.
XX
PR 05-NOV-1998; 98US-0107185P.
XX
PA (UNIV-) UNIV OREGON STATE.
XX
PI Ream W, Mok MC, Lee H;
XX
DR WPI; 2000-365599/31.
XX
PT Gall resistant plants generated by transforming cells with an
PT untranslatable nucleic acid homologous to a gall disease-causing gene.
XX
PS Claim 2; Page 46; 49pp; English.

XX
XX The patent discloses a method for producing plants resistant to gall
XX disease, induced by Agrobacterium infection, by transformation with a
XX bacterial resistance (BR) construct capable of eliciting co-suppression.
XX CC The construct encodes an untranslatable RNA molecule, that is highly
XX CC homologous to the tumour or gall disease-causing genes iaam, iaah and ipt
XX CC of Agrobacterium tumefaciens. These oncogenes are modified by
XX CC introduction of premature termination codons or frameshift mutations, to
XX CC inhibit their expression. This method is used to reduce susceptibility of
XX CC plants to gall diseases. The present DNA sequence is the Agrobacterium
XX CC tumefaciens T-DNA (transferred DNA) gene ipt, required for cytokinin
XX CC production. It encodes an enzyme that converts adenosine monophosphate
XX CC (AMP) into isopentenyl adenosine monophosphate, a cytokinin. The
XX CC overproduction of these plant growth hormones results in gall formation

SQ Sequence 723 BP; 190 A; 175 C; 187 G; 171 T; 0 U; 0 Other;

Query Match 22.5%; Score 714.8; DB 3; Length 723;
Best Local Similarity 99.7%; Pred. No. 5.5e-111;

Matches	716;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
QY	2187	CCTGCATCTAATTTTCGGTCCAACTTGACAGGAAAGACGACCGCGATAGCTCTTGC							2246
Db	6	CCTGCATCTAATTTTCGGTCCAACTTGACAGGAAAGACGACCGCGATAGCTCTTGC							65
QY	2247	CCAGCAGACAGGGCTTCCAGTCTTTCGCTTGATCGGGTCCATCGTCTCTCACTATC							2306
Db	66	CCAGCAGACAGGGCTTCCAGTCTTTCGCTTGATCGGGTCCATCGTCTCTCACTATC							125
QY	2307	AACCGAAGCGGACGACCAACAGTGAAGAACTGAAAGAGACGCGCTCTCACTTGA							2366
Db	126	AACCGAAGCGGACGACCAACAGTGAAGAACTGAAAGAGACGCGCTCTCACTTGA							185
QY	2367	TGATCGGCTCTGTGTGAGGGTATCATCGCAGCCAGCAAGCTCATATAGGCTGATCGA							2426
Db	186	TGATCGGCTCTGTGTGAGGGTATCATCGCAGCCAGCAAGCTCATATAGGCTGATCGA							245
QY	2427	GGAGTGTATATCATGAGGCCAACGGCGGGCTTATCTTTGAGGAGGATCCACCTCGTT							2486
Db	246	GGAGTGTATATCATGAGGCCAACGGCGGGCTTATCTTTGAGGAGGATCCACCTCGTT							305
QY	2487	GCTCAACTGCATGCGCGGAAACAGCTATTTGAGTGCAGATTTTGGTGGCATATATTCCG							2546
Db	306	GCTCAACTGCATGCGCGGAAACAGCTATTTGAGTGCAGATTTTGGTGGCATATATTCCG							365
QY	2547	CCACAAGTTACCCGACCAAGAGACCTTCATGAAAGCGGCCCAAGGCCAGAGTTAAGCAGAT							2606
Db	366	CCACAAGTTACCCGACCAAGAGACCTTCATGAAAGCGGCCCAAGGCCAGAGTTAAGCAGAT							425
QY	2607	GTTGACCCCGGTGACAGGCCATTTCTATTAATCAAGAGTTGTTTATCTTTGGAATGAACC							2666
Db	426	GTTGACCCCGGTGACAGGCCATTTCTATTAATCAAGAGTTGTTTATCTTTGGAATGAACC							485
QY	2667	TGCGCTGAGGCCCATTTCTGAAAAGAGATCGATGATATGCCATGTTGTTGCTAG							2726
Db	486	TGCGCTGAGGCCCATTTCTGAAAAGAGATCGATGATATGCCATGTTGTTGCTAG							545
QY	2727	CCAGAACCAGATCAAGGAGATATGCTATTTGCAAGCTTGACGCCAATATGGAAGTAAGTT							2786
Db	546	CCAGAACCAGATCAAGGAGATATGCTATTTGCAAGCTTGACGCCAATATGGAAGTAAGTT							605
QY	2787	GATTATGGATCGCTCAGAGATATTTTCATTCATGCGCGCCAAACAGAGAAAGAAATTCCTC							2846
Db	606	GATTATGGATCGCTCAGAGATATTTTCATTCATGCGCGCCAAACAGAGAAAGAAATTCCTC							665
QY	2847	CCAAGTTAACGACGCGCTTTCAGAGGATTCGAAGGTCAATCCGTTCCGAATGTATTAG							2904
Db	666	CCAAGTTAACGACGCGCTTTCAGAGGATTCGAAGGTCAATCCGTTCCGAATGTATTAG							723
RESULT 9									
AAD00624 standard; DNA; 747 BP.									
ID AAD00624;									
AC AAD00624;									
DT 29-AUG-2000 (first entry)									
DE Agrobacterium tumefaciens T-DNA mutant ipt gene.									
XX iaam; iaah; ipt; T-DNA; transferred DNA; gall-disease resistance; BR;									
KW bacterial resistance construct; untranslated RNA; tumour; oncogene;									
KW cytokinin; plant growth hormone; mutant; ds.									
OS Agrobacterium tumefaciens.									
XX WO200026346-A1.									
XX 11-MAY-2000.									
XX 04-NOV-1999; 99WO-US026100.									

PR	05-NOV-1998;	98US-0107185P.
XX	(UYOR-) UNIV OREGON STATE.	
XX	Ream W, Mok MC, Lee H;	
XX	WPI; 2000-365599/31.	
DR	Gall resistant plants generated by transforming cells with an	
XX	untranslatable nucleic acid homologous to a gall disease-causing gene.	
PT	Example c; Page 43; 49pp; English.	
XX	The patent discloses a method for producing plants resistant to gall	
CC	disease, induced by Agrobacterium infection, by transformation with a	
CC	bacterial resistance (BR) construct capable of eliciting co-suppression.	
CC	The construct encodes an untranslatable RNA molecule, that is highly	
CC	homologous to the tumour or gall disease-causing genes iaam, iaah and ipt	
CC	of Agrobacterium tumefaciens. These oncogenes are modified by	
CC	introduction of premature termination codons or frameshift mutations, to	
CC	inhibit their expression. This method is used to reduce susceptibility of	
CC	plants to gall diseases. The present DNA sequence is the Agrobacterium	
CC	tumefaciens T-DNA (transferred DNA) mutant ipt gene. The wild type ipt	
CC	gene was modified by deletion of 5' cytosine of the third codon and	
CC	substitution of 3' guanine of the third codon with an adenine. This	
CC	sequence was used for the construction of double stranded RNA and	
CC	untranslatable dsRNA vectors, that reduce gall formation in transformed	
CC	plant cells	
XX	Sequence 747 BP; 198 A; 178 C; 192 G; 179 T; 0 U; 0 Other;	
XX	Query Match	
XX	Best Local Similarity 99.6%; Pred. No. 1.5e-110;	
XX	Matches 714; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY	2188 CTGCATCTAATTTTCGGTCCAACTTGACAGGAAAGACGACCGGATAGCTCTTGGC	2247
Db	18 CTGAATCTAATTTTCGGTCCAACTTGACAGGAAAGACGACCGGATAGCTCTTGGC	77
QY	2248 CAGCAGACAGGGCTTCCAGTCTTTCGCTTGATCGGGTCCAACTGCTCTCACTATCA	2307
Db	78 CAGCAGACAGGGCTTCCAGTCTTTCGCTTGATCGGGTCCAACTGCTCTCACTATCA	137
QY	2308 ACCGGAAGCGGACGACCAACAGTGAAGAACTGAAAGGAAACGCGCTCTACCTTGAT	2367
Db	138 ACCGGAAGCGGACGACCAACAGTGAAGAACTGAAAGGAAACGCGCTCTACCTTGAT	197
QY	2368 GATCGGCTCTGTGTGAGGGTATCATCGCAGCCAAAGCTCATATAGGCTGATCGAG	2427
Db	198 GATCGGCTCTGTGTGAGGGTATCATCGCAGCCAAAGCTCATATAGGCTGATCGAG	257
QY	2428 GAGGTATATATCATGAGGCCAACGGCGGCTTATCTTGAGGGAGATCCACTCGTGG	2487
Db	258 GAGGTATATATCATGAGGCCAACGGCGGCTTATCTTGAGGGAGATCCACTCGTGG	317
QY	2488 CTCACTGCATGGCGGCGGAAACAGCTATTTGAGTGCAGATTTTGGCATATATTGCG	2547
Db	318 CTCACTGCATGGCGGCGGAAACAGCTATTTGAGTGCAGATTTTGGCATATATTGCG	377
QY	2548 CACAAGTTACCCGACCAAGAGACCTTCATGAAGCGGCCAAGGCCAGATTAAAGCAGATG	2607
Db	378 CACAAGTTACCCGACCAAGAGACCTTCATGAAGCGGCCAAGGCCAGATTAAAGCAGATG	437
QY	2608 TTGCACCCCGCTGCAGGCCATTTATATTCAGAGTTGGTTATCTTTGGAATGAACCT	2667
Db	438 TTGCACCCCGCTGCAGGCCATTTATATTCAGAGTTGGTTATCTTTGGAATGAACCT	497
QY	2668 CGGCTGAGGCCCATTTGAAAGAGATCGATGATATCGATATGCCATGTTGTTGCTAGC	2727
Db	498 CGGCTGAGGCCCATTTGAAAGAGATCGATGATATCGATATGCCATGTTGTTGCTAGC	557
QY	2728 CAGAACCAGATCAGCGCAGATATGCTATTGACGCTTGAAGCAATATGGAAGTAAGTTG	2787

PR 29-MAR-1995; 95US-00413135.
XX (WISC) WISCONSIN ALUMNI RES FOUND.
PA
XX Amasino RM, Gan S, Noh Y;
PI
XX WPI; 2002-291012/33.
DR
XX Novel senescence associated promoter sequence connected to a protein-
PT coding DNA sequence useful for the creation of transgenic plants with
PT altered senescence characteristics.
PS
XX Example; Col 17-20; 21pp; English.
XX
XX The invention relates to a genetic construct comprising senescence
CC specific promoter, preferably senescence associated gene (SAG)-12
CC promoter operably connected to a protein-coding DNA sequence not natively
CC connected to the promoter. The senescence associated promoters are useful
CC for the creation of transgenic plants with altered senescence
CC characteristics. Genetic constructs can be inserted into plants which
CC become effective only upon plant cells entering senescence. For example,
CC a gene encoding a biosynthetic enzyme under the control of a senescence-
CC specific promoter can be inserted into a plant, without having the
CC tissues of the plant exposed to the excess of cytokinin during pre-
CC senescence growth. Then at the onset of senescence, the senescence-
CC specific promoter activates cytokinin production to alter the progression
CC of senescence in the plant. The present sequence is Arabidopsis thaliana
CC truncated SAG12 promoter
XX
XX Sequence 709 BP; 279 A; 110 C; 86 G; 234 T; 0 U; 0 Other;
SQ

Query Match 22.3%; Score 709; DB 6; Length 709;
Best Local Similarity 100.0%; Pred. No. 5.2e-110;
Matches 709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1472 AAGCTTTAACTGACGAAATGGTCTCTGTAATAACAGAACTTTGAATTCAAACT 1531
DB 1 AAGCTTTAACTGACGAAATGGTCTCTGTAATAACAGAACTTTGAATTCAAACT 60
QY 1532 ATTTGATTAGTGAAGAAAGAAAGATTCCTGTTTATGTGATTAGATTGAT 1591
DB 61 ATTTGATTAGTGAAGAAAGAAAGATTCCTGTTTATGTGATTAGATTGAT 120
QY 1592 GCATGAAGGTACTACCTACTACAGAGAAATAACATGTACGTAACGATCAGCA 1651
DB 121 GCATGAAGGTACTACCTACTACAGAGAAATAACATGTACGTAACGATCAGCA 180
QY 1652 TGTAAAGTATTTTTTCCAAATTAATTATACATGATAGATTTTTTTTGAATG 1711
DB 181 TGTAAAGTATTTTTTCCAAATTAATTATACATGATAGATTTTTTTTGAATG 240
QY 1712 TCAATTAATAATGCTTCTTAATATTAAATTAAATTAAATAAGGAAATATATTTA 1771
DB 241 TCAATTAATAATGCTTCTTAATATTAAATTAAATTAAATAAGGAAATATATTTA 300
QY 1772 TGCAAAACATCATCAACACATATCCAACTTCGAAATCTCTATAGTACACAGTAGAGAA 1831
DB 301 TGCAAAACATCATCAACACATATCCAACTTCGAAATCTCTATAGTACACAGTAGAGAA 360
QY 1832 AATAAATTTTACTAGATCAAACTTCTCATCATCAATTAATAATGTTTACAAAATAAT 1891
DB 361 AATAAATTTTACTAGATCAAACTTCTCATCATCAATTAATAATGTTTACAAAATAAT 420
QY 1892 TAAACCCACCACTAAATTAATAATAATCCGAGCAAAAGTAGTGAACAAGCTTGATTT 1951
DB 421 TAAACCCACCACTAAATTAATAATAATCCGAGCAAAAGTAGTGAACAAGCTTGATTT 480
QY 1952 CAGGTGATGTAGAGCTAAATGGCTACGTATCAAAACATCAACGATCATTAGTATGTA 2011
DB 481 CAGGTGATGTAGAGCTAAATGGCTACGTATCAAAACATCAACGATCATTAGTATGTA 540
QY 2012 TGAATGAATGTAGTCAATCTGTAATAACAAAATGCTTTGATTGGATCAATCACTTCA 2071

DB 541 TGAATGAATGTAGTCAATCTGTAATAACAAAATGCTTTGATTGGATCAATCACTTCA 600
QY 2072 TGTGAACATTAGCAATTAATCAACCTTATTTTCACTATTAACCCCATCTAGTACCCT 2131
DB 601 TGTGAACATTAGCAATTAATCAACCTTATTTTCACTATTAACCCCATCTAGTACCCT 660
QY 2132 TGTGAAGTATCAATTAAGAGCAAAAGTCAATTAATCTTCTTAAACC 2180
DB 661 TGTGAAGTATCAATTAAGAGCAAAAGTCAATTAATCTTCTTAAACC 709

RESULT 12
AAN70790
ID AAN70790 standard; DNA; 723 BP.
XX
XX AAN70790;
AC
XX 25-MAR-2003 (revised)
DT 03-OCT-2002 (revised)
DT 19-MAR-1991 (first entry)
XX
XX Sequence of tmr gene found in the Eco RI fragment of the Agrobacterium
DE tumefaciens Ti plasmid.
XX
XX Cytokinin biosynthetic enzyme; trans-zeatin; phytohormone; ss.
XX Unidentified.
XX
XX Key Location/Qualifiers
FH 1-.723
FT CDS /*tag= a
FT
XX
XX AUN8770154-A.
PN
XX 24-SEP-1987.
PD
XX 18-MAR-1987; 87AU-00070154.
PF
XX 19-MAR-1986; 86US-00841464.
PR 11-APR-1986; 86US-00850963.
PR
XX (UYOR-) UNIV OREGON STATE.
PA
XX Morris RO, Regier DA;
PI
XX WPI; 1987-313994/45.
DR P-PSDB; AAP70484.
DR
XX
XX New recombinant DNA molecules - for prodn. of cytokinin(s) in good yields
PT by cultivating Escherichia coli transformants.
PT
XX
XX Example; Fig 5; 59pp; English.
PS
XX tmr is a designation for a gene which codes for a cytokinin biosynthetic
CC enzyme and which can be found in the EcoRI fragment of the Agrobacterium
CC tumefaciens Ti plasmid. tzs is a designation for a gene which codes for a
CC cytokinin biosynthetic enzyme and which can be found in or near the vir
CC region of the Agrobacterium tumefaciens Ti plasmid pTiC58. ptz is a
CC designation for a gene which codes for a cytokinin biosynthetic enzyme
CC and which can be found in the larger (105 kb) plasmid of P. savastanoi
CC strain 1006. When tmr and tzs are included in the same plasmid, there is
CC a good increase in trans-zeatin yield. (Updated on 03-OCT-2002 to add
CC missing OS field.) (Updated on 25-MAR-2003 to correct PF field.) (Updated
CC on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 723 BP; 191 A; 175 C; 186 G; 171 T; 0 U; 0 Other;
SQ

Query Match 22.0%; Score 701.2; DB 1; Length 723;
Best Local Similarity 99.4%; Pred. No. 1.1e-108;
Matches 714; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 2188 CTGCATCTAATTTCCGTCGAACCTGCACAGG-AAAGACGACGACCGGATAGCTCTTGC 2246

Db 6 CTGCATCTAATTTTCGGTCCAACTGCACAGAAAGACGACGCCGATAGCTCTTGC 65
QY 2247 CCAGCAGACAGGGCTTCCAGTCTTTCGTTGATCGGGTCCAATCGTCTCAACTATC 2306
Db 66 CCAGCAGACAGGGCTTCCAGTCTTTCGTTGATCGGGTCCAATCGTCTCAACTATC 125
QY 2307 AACCGAAGCGGACGACCAACAGTGAAGAACTGAAAGGAAACGACGCCGTCTTACCTGA 2366
Db 126 AACCGAAGCGGACGACCAACAGTGAAGAACTGAAAGGAAACGACGCCGTCTTACCTGA 185
QY 2367 TGATCGGCTCTGTGGAGGGTATCATCGCAGCCAAAGCTCATAGGCTGATCGA 2426
Db 186 TGATCGGCTCTGTGGAGGGTATCATCGCAGCCAAAGCTCATAGGCTGATCGA 245
QY 2427 GGAGGTGTATATCATGAGCCCAACGCGGCTTATTTCTGAGGAGATCCACTCGTT 2486
Db 246 GGAGGTGTATATCATGAGCCCAACGCGGCTTATTTCTGAGGAGATCCACTCGTT 305
QY 2487 GCTCACTGCATGGCGGCAACAGCTATTGAGTGCAGATTTTCTGGCAATATTTCG 2546
Db 306 GCTCACTGCATGGCGGCAACAGCTATTGAGTGCAGATTTTCTGGCAATATTTCG 365
QY 2547 CCACAACTTACCCGACCAAGACACTTTCATGAAAGCGGCCAAGCCAGAGTTAAGCAT 2606
Db 366 CCACAACTTACCCGACCAAGACACTTTCATGAAAGCGGCCAAGCCAGAGTTAAGCAT 425
QY 2607 GTTGACACCCCGCTGCAGGCCCATTTCTATTATCAAGAGTTGTTTATCTTTGAATGAAC 2666
Db 426 GTTGACACCCCGCTGCAGGCCCATTTCTATTATCAAGAGTTGTTTATCTTTGAATGAAC 485
QY 2667 TCGGCTGAGGCCCATTTCTGAAAGAGATCGATGATATCGATATGCCATGTTGTTGCTAG 2726
Db 486 TCGGCTGAGGCCCATTTCTGAAAGAGATCGATGATATCGATATGCCATGTTGTTGCTAG 545
QY 2727 CCAGAACAGATCAACGACAGATATGCTATTGACAGCTTGAACCAATATGGAAGTAAGTT 2786
Db 546 CCAGAACAGATCAACGACAGATATGCTATTGACAGCTTGAACCAATATGGAAGTAAGTT 605
QY 2787 GATTAATGGGATCGCTCAGAGATATTCATCCATGCGGCCAACAGAAATATCC 2846
Db 606 GATTAATGGGATCGCTCAGAGATATTCATCCATCCGCCAACAGAAATATCC 665
QY 2847 CCAAGTTAACGACGCCGCTTTCGACCGGATTCGAAGGTCAATCCGTTCCGAATGTATTAG 2904
Db 666 CCAAGTTAACGACGCCGCTTTCGACCGGATTCGAAGGTCAATCCGTTCCGAATGTATTAG 723

RESULT 13
AAD44425
ID AAD44425 standard; DNA; 613 BP.
XX
AC AAD44425;
XX
DT 13-DEC-2002 (first entry)
XX
DE PGL471 construct comprising SAG12-35S promoter DNA.
XX
KM Cauliflower mosaic virus 35S RNA; 35S; promoter; transgenic plant; OPR;
KM peanut chlorotic streak caulimovirus full length transcript promoter;
KM PCISV; 12-oxophytodienoic acid-100, 11-reductase gene promoter; SAG12;
KM transgenic; CamV; chimeric; ds.
XX
OS Cauliflower mosaic virus.
OS Unidentified.
OS Chimeric.
XX
PN US6388170-B1.
XX
PD 14-MAY-2002.
XX
PF 07-APR-2000; 2000US-00545244.
XX
PR 07-APR-2000; 2000US-00545244.

XX
PA (KENT) UNIV KENTUCKY RES FOUND.
XX
PI Gan S, Xie M, He Y;
XX
DR WPI; 2002-442888/47.
XX
PT Bi-directional promoter with common promoter linked in opposite
PT orientation to minimal promoter, useful to direct expression of
PT polynucleotide which confers agronomically significant trait to
PT transgenic plant.
XX
PS Disclosure; Col 15-16; 16pp; English.
XX
CC The invention relates to an artificial nucleic acid construct comprising
CC a bi-directional promoter having a minimal promoter operably linked in
CC opposite orientation 5' to a common promoter, where each promoter is
CC either cauliflower mosaic virus (CaMV) 35S RNA promoter (35S), peanut
CC chlorotic streak caulimovirus full length transcript promoter (PCISV),
CC Arabidopsis 12-oxophytodienoic acid-100, 11-reductase gene promoter (OPR)
CC or SAG12, and where each end of the bi-directional promoter is operably
CC linked to a polynucleotide encoding a polypeptide. The construct is used
CC to produce a transgenic plant which has an agronomically-significant
CC trait. The present sequence is PGL471 construct comprising SAG12-35S
CC promoter DNA
XX
SQ Sequence 613 BP; 241 A; 100 C; 64 G; 208 T; 0 U; 0 Other;
Query Match. 17.9%; Score 569.4; DB 6; Length 613;
Best Local Similarity 99.8%; Pred. No. 1.4e-86;
Matches 570; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1604 CCTACGTACTACAGAAATAAATACATGTACGTAACTACGTATCAGCATGTAAAGTATT 1663
Db 5 CTACGTACTACAGAAATAAATACATGTACGTAACTACGTATCAGCATGTAAAGTATT 64
QY 1664 TTTTTCCTTAATATTATTAATTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1723
Db 65 TTTTTCCTTAATATTATTAATTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 124
QY 1724 GCTTCTTAATATTATTTAATTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1783
Db 125 GCTTCTTAATATTATTTAATTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 184
QY 1784 TCAACACATATCCAACTTGAAGAAATCTCTATAGTACACAGTAAGAAATAATTTTAC 1843
Db 185 TCAACACATATCCAACTTGAAGAAATCTCTATAGTACACAGTAAGAAATAATTTTAC 244
QY 1844 TAGATTAACAACCTCTCAATCATCAATTATTAATTTTACAAACTAATTAACCCACAC 1903
Db 245 TAGATTAACAACCTCTCAATCATCAATTATTAATTTTACAAACTAATTAACCCACAC 304
QY 1904 TAAATTAATAAATAATCCGACAAAGTGAAGTAAGTAAGTATTCAGGTTGATGTA 1963
Db 305 TAAATTAATAAATAATCCGACAAAGTGAAGTAAGTAAGTATTCAGGTTGATGTA 364
QY 1964 GGACTTAAATGGCTACGTATCAACATCAACGATCATTTAGTTATGTATGAATGTA 2023
Db 365 GGACTTAAATGGCTACGTATCAACATCAACGATCATTTAGTTATGTATGAATGTA 424
QY 2024 GTCATTACTGTAAACAAATAATGCTTTGATTTGGATCAATCACTTCATGTGAACATTAG 2083
Db 425 GTCATTACTGTAAACAAATAATGCTTTGATTTGGATCAATCACTTCATGTGAACATTAG 484
QY 2084 CAATTACATCAACCTTATTTTACATTAATAAACCCCATCTCAGTACCTTCTGAAGTATC 2143
Db 485 CAATTACATCAACCTTATTTTACATTAATAAACCCCATCTCAGTACCTTCTGAAGTATC 544
QY 2144 AAATTAGAGCAAAAGTCATTTAATCTTCT 2174
Db 545 AAATTAGAGCAAAAGTCATTTAATCTTCT 575

RESULT 14
AAC86511
ID AAC86511 standard; DNA; 3017 BP.
XX AC AAC86511;
XX AC AAC86511;
DT 19-MAR-2001 (first entry)
XX
XX DNA construct comprising a maize promoter and Agrobacterium ipt gene.
DE
XX
XX temporal gene expression; spatial gene expression; plant seed;
KW cytokinin modulating gene; transgenic plant; seed size; stress tolerance;
KW yield stability; tip kernel abortion; seed set; isopentenyl transferase;
KW ipt; ss.
XX
OS Synthetic.
OS Zea mays.
OS Agrobacterium tumefaciens.
XX
XX WO200063401-A1.
PD 26-OCT-2000.
XX
PF 13-APR-2000; 2000WO-US009943.
XX
PR 16-APR-1999; 99US-0129844P.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Habben JE, Zinselmeier C, Tomes D;
XX
XX WPI; 2000-672743/65.
DR
XX
XX Novel recombinant DNA construct useful for producing transgenic plants
PT having enhanced levels of cytokinin expression, improved stress tolerance
PT and yield stability.
XX
PS Disclosure; Page 72-73; 76pp; English.
XX
XX The present sequence represents a recombinant DNA molecule of the
CC invention. It comprises, in this order, a maize promoter, an
CC Agrobacterium isopentenyl transferase (ipt) gene fragment, and a maize
CC terminator. The DNA molecules of the invention comprise a genetic
CC construct consisting of a promoter directing temporal and/or spatial gene
CC expression in plant seed operatively linked to a cytokinin modulating
CC gene. The recombinant DNA molecules are useful for producing fertile,
CC transgenic plants capable of regulated expression of a cytokinin
CC modulating gene in developing seeds. They are also useful for improving
CC stress tolerance and yield stability in plants. The preferential
CC expression of recombinant DNA molecules of the invention occurs about 14-
CC 25 days after pollination. The transgenic plants thus produced have
CC enhanced levels of cytokinin expression exhibit improved seed size,
CC decreased tip kernel abortion and increased seed set during unfavourable
CC environmental conditions
XX
SQ Sequence 3017 BP; 865 A; 679 C; 622 G; 851 T; 0 U; 0 Other;

Query Match 16.9%; Score 536.4; DB 3; Length 3017;
Best Local Similarity 83.9%; Pred. No. 5.3e-81;
Matches 606; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 2178 ACCATGACCCCTGCATCTAATTTTGGTCCAACTTGACAGGAAAGACGACGCCGAT 2237
DB 1404 AACAAATGATCTACGTCTAATTTTGGTCCAACTTGACAGGAAAGACATCGACTGCCAT 1463
QY 2238 AGCTCTTGCCCGACAGACAGAGGCTTCCAGTCTTTCGCTTGATCGGGTCCAATCGTGTCC 2297
DB 1464 AGCTCTTGCCCGACAGACTGGCTTCCAGTCTTTCGCTTGATCGGGTCCAATCGTGTCC 1523
QY 2298 TCAACTATCAACCGAAGCGAGCAACCAAGTGAAGAACTGAAGGAAGCAAGCGCTCT 2357
DB 1524 TCAACTATCAACCGAAGCGGCGGCGACCAACAGTGAAGAACTGAAGGAAGCAAGCGCTCT 1583

QY 2358 CTACCTGATGATCGGCTCTGTGAGGGTATCATCGACGCCAAGCAAGCTCATATAG 2417
DB 1584 GTACCTGATGATCGGCTTGTGTAAGGGTATCATACAGCCAAAGCTCATGAACG 1643
QY 2418 GCTGATCGAGGAGGTGTAATCATATGAGGCCAAGCGGGCTTATCTTGAGGAGGATC 2477
DB 1644 GCTCATGCGAGGTGCAATCATCAGAGGCCAAAGCGGGCTTATCTTGAGGAGGATC 1703
QY 2478 CACCTGTTGCTCAACTGCATGCGCGGAAACAGCTATTGGAGTGCAGATTTTCGTGGCA 2537
DB 1704 TATCTGTTGCTCAGGTGATGCGCAAGGCTGTAATTGGAACGCGGATTTTCGTGGCA 1763
QY 2538 TATTATTCGCCACAAGTTAACCCGACCAAGAGACCTTCATGAAAAGCGCCAAAGCGCAGAT 2597
DB 1764 TATTATTCGCAACGAGTTAGCAGACGAGAGAGCTTCATGAGCGTGCCAAAGACCAAGAT 1823
QY 2598 TAAGCAGATGTTGACCCCGCTGCAGGCCATTTCTATTATCAAGAGTTGTTATCTTTG 2657
DB 1824 TAAGCAGATGTTACGCCCCCTCTGACAGTCTTTCTATTATCAAGAGTTGTTCAACTTTG 1883
QY 2658 GAATGAACCTCGGCTGAGGCCCATTTCTGAAGAGATCGATGATATCGATATGCCATGTT 2717
DB 1884 GAGGAGACCTCGGCTGAGGCCCATTAATCGAAGGATCGATGATATCGATATGCCATGTT 1943
QY 2718 GTTTGCTAGCCAGAACCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2777
DB 1944 ATTTGCTACCCAGAACCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2803
QY 2778 AGGTAAGTGTATTATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 2837
DB 2004 GAATAAATTGATTCACGATGATGATGATGATGATGATGATGATGATGATGATGAT 2863
QY 2838 GAAATTCCTCCCAAGTTAACGACGCGCTTTCGACGATTCGAAAGTTCATCCGTTCCGAT 2897
DB 2064 GAAATTCCTTGTGTTGGCGGCGACGCTGTGGAAGCGTTTGAAGACCAACATTTGGAAT 2123
QY 2898 GT 2899
DB 2124 GT 2125

RESULT 15
AAC86514
ID AAC86514 standard; DNA; 721 BP.
XX
XX AAC86514;
AC
DT 19-MAR-2001 (first entry)
XX
XX Nucleotide sequence of an isopentenyl transferase (ipt) gene fragment.
DE
XX
XX temporal gene expression; spatial gene expression; plant seed;
KW cytokinin modulating gene; transgenic plant; seed size; stress tolerance;
KW yield stability; tip kernel abortion; seed set; isopentenyl transferase;
KW ipt; ss.
XX
XX Agrobacterium tumefaciens.
OS
XX
XX WO200063401-A1.
PN
XX
XX 26-OCT-2000.
PD
XX
XX 13-APR-2000; 2000WO-US009943.
PF
XX
XX 16-APR-1999; 99US-0129844P.
PR
XX
XX (PION-) PIONEER HI-BRED INT INC.
PA
XX
XX Habben JE, Zinselmeier C, Tomes D;
PI
XX
XX WPI; 2000-672743/65.
DR
XX
XX Novel recombinant DNA construct useful for producing transgenic plants

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OM nucleic - nucleic search, using SW model

Run on: June 9, 2004, 22:40:04 ; Search time 249 Seconds
(without alignments)
7094.011 Million cell updates/sec

Title: US-10-072-077A-1
Perfect score: 3183
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3183	100.0	3183	1	US-08-413-135-1	Sequence 1, Appli
2	3171	99.6	3182	4	US-08-971-395-1	Sequence 1, Appli
3	734.8	23.1	745	3	US-09-073-587-4	Sequence 4, Appli
4	733.4	23.0	24595	6	5428147-1	Patent No. 5428147
5	709	22.3	709	1	US-08-413-135-2	Sequence 2, Appli
6	709	22.3	709	4	US-08-971-395-2	Sequence 2, Appli
7	569.4	17.9	613	4	US-09-545-244A-11	Sequence 11, Appli
8	344.4	10.8	584	1	US-08-054-985-2	Sequence 2, Appli
9	257.2	8.1	1829	1	US-07-966-187-17	Sequence 17, Appli
10	257.2	8.1	1863	1	US-08-525-507-16	Sequence 16, Appli
11	257.2	8.1	1863	2	US-07-842-165-9	Sequence 9, Appli
12	257.2	8.1	1863	2	US-07-842-165-9	Sequence 9, Appli
13	257.2	8.1	4284	1	US-08-525-507-14	Sequence 14, Appli
14	256.2	8.0	15397	2	US-08-673-768-1	Sequence 1, Appli
15	256.2	8.0	15397	2	US-08-673-768-1	Sequence 1, Appli
16	256	8.0	2633	1	US-08-452-267-2	Sequence 2, Appli
17	256	8.0	2633	3	US-09-123-644-2	Sequence 2, Appli
18	256	8.0	5534	1	US-08-452-267-3	Sequence 3, Appli
19	256	8.0	5534	3	US-09-123-644-3	Sequence 3, Appli
20	255	8.0	6548	3	US-08-894-440-1	Sequence 1, Appli
21	255	8.0	6548	3	US-08-817-188-2	Sequence 2, Appli
22	255	8.0	6548	4	US-09-458-093-1	Sequence 1, Appli
23	254.2	8.0	2709	4	US-09-319-275A-12	Sequence 12, Appli
24	253.2	8.0	9299	4	US-09-097-319A-15	Sequence 15, Appli
25	253.2	8.0	9335	4	US-09-097-319A-19	Sequence 19, Appli
26	253.2	8.0	10160	4	US-09-097-319A-8	Sequence 8, Appli
27	253.2	8.0	11784	4	US-09-097-319A-9	Sequence 9, Appli

28	253.2	8.0	11991	4	US-09-097-319A-10	Sequence 10, Appli
29	253	7.9	2115	2	US-08-767-026-3	Sequence 3, Appli
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31	252.8	7.9	10249	4	US-09-186-002-14	Sequence 14, Appli
32	252.8	7.9	10252	4	US-09-186-002-15	Sequence 15, Appli
33	252.8	7.9	10339	4	US-09-186-002-13	Sequence 13, Appli
34	252.6	7.9	3237	2	US-08-419-075-26	Sequence 26, Appli
35	252.6	7.9	14194	4	US-09-577-424-3	Sequence 3, Appli
36	252.2	7.9	1138	4	US-09-011-151-8	Sequence 8, Appli
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38	252.2	7.9	1630	4	US-09-441-340-23	Sequence 23, Appli
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43	252.2	7.9	5592	4	US-09-495-797-37	Sequence 37, Appli
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ALIGNMENTS

RESULT 1
US-08-413-135-1
; Sequence 1, Application US/08413135
; Patent No. 5689042
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard M
; TITLE OF INVENTION: Transgenic Plants with Altered
; TITLE OF INVENTION: Senescence Characteristics
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/413,135
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 960296.92808
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3183 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "SAG12-1 Promoter DNA"
; US-08-413-135-1

Query Match 100.0%; Score 3183; DB 1; Length 3183;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATATCTCTTTTATATCAACATAAGTGTGAGATATGTTGAGAAGAGACAATATT 60
Db 1 GATATCTCTTTTATATCAACATAAGTGTGAGATATGTTGAGAAGAGACAATATT 60

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Db	61	CTCGTGAGCACCCGAGCTCTGTTTATATATAGAAAACCCGATTGTTATTTTGTAGACTGAGAC	120
QY	121	AAAAAGTAAATCGTTGATGTGTAATAATTTAAATTAGTTTCATCAGTTTCGATTAATA	180
Db	121	AAAAAGTAAATCGTTGATGTGTAATAATTTAAATTAGTTTCATCAGTTTCGATTAATA	180
QY	181	AAATGATTTAGTTATCATAGCTATATATAGCATGATTCTAAATTGTTTTTGTACACCCCTT	240
Db	181	AAATGATTTAGTTATCATAGCTATATATAGCATGATTCTAAATTGTTTTTGTACACCCCTT	240
QY	241	TTTTCTCTCTTTGGTGTGTTTCTTAACATTTAGAAAGAACCCATTAACATGTACGTTCAAA	300
Db	241	TTTTCTCTCTTTGGTGTGTTTCTTAACATTTAGAAAGAACCCATTAACATGTACGTTCAAA	300
QY	301	AATTAAAAACAATATTTCCAAAGTTTATATATACGAAACCTGTTTTTTTAAATGAAACACAG	360
Db	301	AATTAAAAACAATATTTCCAAAGTTTATATATACGAAACCTGTTTTTTTAAATGAAACACAG	360
QY	361	GAATAGTTGATTTATGAAATTTAGTAGATCAATATATGATCAATGATGATATATAT	420
Db	361	GAATAGTTGATTTATGAAATTTAGTAGATCAATATATGATCAATGATGATATATAT	420
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Db	421	ATGAACCTCAGTTGTTATATACAGAAATGAAATGCTATTTAAATACCGATCATGAAGTGT	480
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Db	481	AAAAAGTGCAGAAATATGACATGAAAGCGTTTGTCTTACCAGGATTCGAGTTATAGTTT	540
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Db	541	GGATCTCTCAAGAAATATTTGGGCCATATTTAGTTATATTTGGGCTTAAGCGTTTTCAAA	600
QY	601	GAGACGAGGAAGAAAGATTGGGTCAGTTTAACAAAACAGAGACACTCGTATTAAGTTGTA	660
Db	601	GAGACGAGGAAGAAAGATTGGGTCAGTTTAACAAAACAGAGACACTCGTATTAAGTTGTA	660
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Db	661	CTTTGGTAGCAAGTCGATTATTTGCCAGTAAAACTTGGTACACAACTGCAACTCGTA	720
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Db	721	TCGTTATTTAGTTTGTACTTGGTACCTTTGGTTAAGAAAAAGTGATATAGTTAAATCAGT	780
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Db	781	TGTGTTCATGAGGTGATTTGTAATTGTTGTAAGGCGATTCTTCACATCAACAA	840
QY	841	TAAACAAGTTTTATAGATTTTTTTTATTAACATTTTTGCCACGCTTCGTAAGTTGTA	900
Db	841	TAAACAAGTTTTATAGATTTTTTTTATTAACATTTTTGCCACGCTTCGTAAGTTGTA	900
QY	901	TTTACACCGCATTTTTTCCCTGTACAGAAATTCATATATATTTATTTATATACCTCAGTT	960
Db	901	TTTACACCGCATTTTTTCCCTGTACAGAAATTCATATATATTTATTTATATACCTCAGTT	960
QY	961	GACAAATTAAGTTTATTAACGTTTATTAACAATTTATTTAAATACCATGTGAAGATCCAGAA	1020
Db	961	GACAAATTAAGTTTATTAACGTTTATTAACAATTTATTTAAATACCATGTGAAGATCCAGAA	1020
QY	1021	TATGTTTACTTCTTCTTTGTGTAGAAAACTAATATATATCACTATATAATAAAAATATCT	1080
Db	1021	TATGTTTACTTCTTCTTTGTGTAGAAAACTAATATATATCACTATATAATAAAAATATCT	1080
QY	1081	AATCATTTATTTGTAAATATGCAAGTTATTTGTCAATTTTGAATTTAGTATTTAGACGG	1140
Db	1081	AATCATTTATTTGTAAATATGCAAGTTATTTGTCAATTTTGAATTTAGTATTTAGACGG	1140

QY	1141	TTATCACTTCAGCCAAATATGATTGGATTAAAGTCCAAAATGCAATTTGTCGATACC	1200
Db	1141	TTATCACTTCAGCCAAATATGATTGGATTAAAGTCCAAAATGCAATTTGTCGATACC	1200
QY	1201	CTCTGTGCTAATGATTATTTCATAATTTCTATATTATCCCTAACTACAGAGCTACA	1260
Db	1201	CTCTGTGCTAATGATTATTTCATAATTTCTATATTATCCCTAACTACAGAGCTACA	1260
QY	1261	TTTATATTGTATTTCTAATGACAGGAACTTTCATAGAGATTGATAGATAAATTGGT	1320
Db	1261	TTTATATTGTATTTCTAATGACAGGAACTTTCATAGAGATTGATAGATAAATTGGT	1320
QY	1321	GGGAAACATCATTTGAACAAGAACTTTAGCAATCATATCGATTATCTACAAAAGAA	1380
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QY	1381	ACTTAGCGTAATGAAGTTCACCTGTGTGAATGCACTATGATTGTATCAAAATTAGTTA	1440
Db	1381	ACTTAGCGTAATGAAGTTCACCTGTGTGAATGCACTATGATTGTATCAAAATTAGTTA	1440
QY	1441	TTGTGGAATCATTTTCTTTTGTATTGATTGAAGCTTTAACTTGCACGAATGGTTCTCT	1500
Db	1441	TTGTGGAATCATTTTCTTTTGTATTGATTGAAGCTTTAACTTGCACGAATGGTTCTCT	1500
QY	1501	TGTGAATAAACAGAAATCTTTGAATTCAAACTATTGATTAGTGAAGAACAAAAGAA	1560
Db	1501	TGTGAATAAACAGAAATCTTTGAATTCAAACTATTGATTAGTGAAGAACAAAAGAA	1560
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Db	1561	TCCTTGTTTTATGTGATTAAGTATTTGTGATGCAAGAAAGTACCTACGTACTACAAGAA	1620
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QY	1861	ATCATCAATTATAAATGTTTACAAACTAATTAAACCACTAAATTTAACTAAAAAT	1920
Db	1861	ATCATCAATTATAAATGTTTACAAACTAATTAAACCACTAAATTTAACTAAAAAT	1920
QY	1921	CCGAGCAAAAGTAGTGAACAAGACTTGATTTTCAGGTTGATGTAGACTAAATGGCTACG	1980
Db	1921	CCGAGCAAAAGTAGTGAACAAGACTTGATTTTCAGGTTGATGTAGACTAAATGGCTACG	1980
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QY	2101	TTTTCACTATAAAACCCCATCTCAGTACCCTTCTGAAGTAATCAAAATTAAAGCAAAAG	2160
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QY	2221	AAGACGACGACCGGATAGCTCTTGCCCAAGCAGACAGGGCTTCCAGTCCCTTTCGTTGAT	2280

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QY 2821 GCGGCCAAGCAAGAAATTCGCCAAGTTAACGACGCGCTTCGACGATTGAA 2880
Db 2821 GCGGCCAAGCAAGAAATTCGCCAAGTTAACGACGCGCTTCGACGATTGAA 2880
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QY 3001 TTCTGTTGAATTAAGTAAATTAAGCATGTAATAATTAACATGTAATGATGAGTTATGA 3060
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QY 3181 TTC 3183
Db 3181 TTC 3183
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RESULT 2
US-08-971-395-1
; Sequence 1, Application US/08971395
; Patent No. 6359197
; GENERAL INFORMATION:
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APPLICANT: Amasino, Richard M
APPLICANT: No. 6359197, Yoo-Sun
APPLICANT: Gan, Susheng
TITLE OF INVENTION: Transgenic Plants with Altered
TITLE OF INVENTION: Senescence Characteristics
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,395
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.94908
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3182 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-971-395-1

Query Match
Best Local Similarity 99.6%; Score 3171; DB 4; Length 3182;
Matches 3182; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 361 GAATAGTTGATTATGAATTAAGTTAGATCAATACTCAATATATGATCAATGATATAT 420
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Db 421 ATGAACCTAGTTGTTATACAAAGAAATGAATGCTATTAAATACCGATCATGAAGTGT 480
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 QY 661 CTTTGGTAGCAAGTCGATTATTTGGCAGTAAAACTTGCTACACAACCTGACAACCTGTA 720
 Db 661 CTTTGGTAGCAAGTCGATTATTTGGCAGTAAAACTTGCTACACAACCTGACAACCTGTA 720
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 Db 721 TCGTATTAGTTTGTACTTGGTACCTTTGGTTAAGAAAAAGTTGATATAGTTAATCAGT 780
 QY 781 TGTGTCATGAGGTGATGTGATTTAATTTGTGACTAGGGCGATTCCTTCACATCACA 840
 Db 781 TGTGTCATGAGGTGATGTGATTTAATTTGTGACTAGGGCGATTCCTTCACATCACA 840
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 Db 1021 TATGCTTACTTCTTCTTGTGTAGAAAACCTAATATCACTATATTAATAATAATAATTCT 1080
 QY 1081 AATCATTATATTGTAAATATGCAAGTTATTTGTCAATTTTGAATTTAGTATTTAGACGG 1140
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 QY 1321 GGGAAACATCATGACAGGAACTTTAGCAAAATCATATCGATTTATCTACAAAAGAA 1380
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 Db 1801 TCGAAATCTCTATAGTACACAAGTAGAGAAATTAATTTTACTAGATACAAACTTCCTA 1860
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 Db 1861 ATCATCAATTTATTAATGTTTACAAAATAATTTAAACCCACCACTAAATACTAAAAAT 1920
 QY 1921 CCGAGCAAGTGAAGTGAACAAGACTTGAATTTCAAGTTGATGTAGAGACTAAATGGCTACG 1980
 Db 1921 CCGAGCAAGTGAAGTGAACAAGACTTGAATTTCAAGTTGATGTAGAGACTAAATGGCTACG 1980
 QY 1981 TATCAACATCAACGATCATTTAGTTATGTATGAATGAATGTAGTCAATTACTGTAAAC 2040
 Db 1981 TATCAACATCAACGATCATTTAGTTATGTATGAATGAATGTAGTCAATTACTGTAAAC 2040
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 Db 2041 AAAAATGCTTGAATTTGATCAATCACTCATGTGAACATTTAGCAATTAATCAACTTA 2100
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 Db 2161 CATTTAATTTCTTAATAAACCATGAGACCTGCATTAATTTTGGTCCAACTTGACACAGA 2220
 QY 2221 AAGACGACGCGGATAGCTCTTGGCCGACAGACAGGGCTTCCAGTCTTCCGCTTGAT 2280
 Db 2221 AAGACGACGCGGATAGCTCTTGGCCGACAGACAGGGCTTCCAGTCTTCCGCTTGAT 2280
 QY 2280 CCGGTCCAATCGTCTCTCACTATCAACCGGAAACCGGACCAACAGTGAAGAACTG 2340
 Db 2280 CCGGTCCAATCGTCTCTCACTATCAACCGGAAACCGGACCAACAGTGAAGAACTG 2340
 QY 2341 AAAAGAACGACGCGTCTCTCACTATCAACCGGAAACCGGACCAACAGTGAAGAACTG 2400
 Db 2341 AAAAGAACGACGCGTCTCTCACTATCAACCGGAAACCGGACCAACAGTGAAGAACTG 2400
 QY 2401 AAGCAAGCTCATCATAGGCTGATCGAGAGGTGTATATCATGAGGCCAACGGCGGCTT 2460
 Db 2401 AAGCAAGCTCATCATAGGCTGATCGAGAGGTGTATATCATGAGGCCAACGGCGGCTT 2460
 QY 2460 AATCTTGAGGAGGATCCACTCTGCTCACTGCACTGCGCGGAAACAGCTATTTGAGT 2519
 Db 2460 AATCTTGAGGAGGATCCACTCTGCTCACTGCACTGCGCGGAAACAGCTATTTGAGT 2519
 QY 2521 GCAGATTTTCTTGGCATATTTTCCGACAGATTAACCCGACCAAGAGACCTTCATGAA 2580
 Db 2521 GCAGATTTTCTTGGCATATTTTCCGACAGATTAACCCGACCAAGAGACCTTCATGAA 2580
 QY 2580 GCGGCCAAGGCGAGATTAAGCAGATGTTGCAACCCGCTGACAGGCCATTTCTATATGCA 2639
 Db 2580 GCGGCCAAGGCGAGATTAAGCAGATGTTGCAACCCGCTGACAGGCCATTTCTATATGCA 2639
 QY 2641 GAGTTGTTTATCTTTGAATGAACCTCGGCTGAGGCCCATTTCTGAAGAGATCGATGGA 2700

DB 2640 GAGTGGTTTATCTTTGGAATGAACCTCGGCTGAGGCCCATTCGAAGAAGATCGATGGA 2699
QY 2701 TATCGATATGCCATGTTGTTGCTAGCCAGAAACAGATCAGCGCAGATATGCTATTGCA 2760
DB 2700 TATCGATATGCCATGTTGTTGCTAGCCAGAAACAGATCAGCGCAGATATGCTATTGCA 2759
QY 2761 CTGACGCAATATGGAAGGTAAGTGAATTAATGGGATCGCTCAGAGTATTTCATCCAT 2820
DB 2760 CTGACGCAATATGGAAGGTAAGTGAATTAATGGGATCGCTCAGAGTATTTCATCCAT 2819
QY 2821 GCGCGCCACAGAGAACAGAAATTCGCCCAAGTTAACGACGCCGCTTCGACGGATTGAA 2880
DB 2820 GCGCGCCACAGAGAACAGAAATTCGCCCAAGTTAACGACGCCGCTTCGACGGATTGAA 2879
QY 2881 GGTGATCCGTTCCGAATGATTAAGTTACGCCAGCCCTGAGCTCGATCTCAACATTT 2940
DB 2880 GGTGATCCGTTCCGAATGATTAAGTTACGCCAGCCCTGAGCTCGATCTCAACATTT 2939
QY 2941 GGCATTAAGTTCTTAAAGATTGAATGATCTGTCGCCGCTTGGCATGATTATCATATAAT 3000
DB 2940 GGCATTAAGTTCTTAAAGATTGAATGATCTGTCGCCGCTTGGCATGATTATCATATAAT 2999
QY 3001 TTCTGTTGAATTAAGTTAAGCATGTAATTAATTAACATGTAATGATGACGTTATTATGA 3060
DB 3000 TTCTGTTGAATTAAGTTAAGCATGTAATTAATTAACATGTAATGATGACGTTATTATGA 3059
QY 3061 GATGGGTTTATGATTAAGTCCCGCAATTATACATTTAATACGGCATAGAAAAACAAA 3120
DB 3060 GATGGGTTTATGATTAAGTCCCGCAATTATACATTTAATACGGCATAGAAAAACAAA 3119
QY 3121 TATGGCGCCGAACGTGGATAATTAATCGCGCGCGGTGTCATCTATGTTACTAGATCGAA 3180
DB 3120 TATGGCGCCGAACGTGGATAATTAATCGCGCGCGGTGTCATCTATGTTACTAGATCGAA 3179
QY 3181 TTC 3183
DB 3180 TTC 3182

RESULT 3
US-09-073-587-4
Sequence 4, Application US/09073587
Patent No. 6268552
GENERAL INFORMATION:
APPLICANT: Li, Yi
TITLE OF INVENTION: Transgenic Seedless Plants
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,587
FILING DATE: 06-MAY-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/045,725
FILING DATE: 06-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 4-97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080

TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..725
US-09-073-587-4

Query Match 23.1%; Score 734.8; DB 3; Length 745;
Best Local Similarity 99.7%; Pred. No. 3.2e-151;
Matches 736; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2187 CCTGATCTAATTTTCGGTCCAACTTGCAAGAAAGACGACCGCATAGCTCTTGC 2246
DB 8 CCTGATCTAATTTTCGGTCCAACTTGCAAGAAAGACGACCGCATAGCTCTTGC 67
QY 2247 CCAGACAGAGGCTTCCAGTCTTTGCTTGTGATCGGGTCCATCTGCTCACTATC 2306
DB 68 CCAGACAGAGGCTTCCAGTCTTTGCTTGTGATCGGGTCCATCTGCTCACTATC 127
QY 2307 AACCGAAGCGGACGACCAACAGTGAAGAACTGAAAGGAACGACCGCTCTACCTGA 2366
DB 128 AACCGAAGCGGACGACCAACAGTGAAGAACTGAAAGGAACGACCGCTCTACCTGA 187
QY 2367 TGATCGGCTCTGTTGAGGGTATCATCGACCCAAAGCTCATAGGCTGATCGA 2426
DB 188 TGATCGGCTCTGTTGAGGGTATCATCGACCCAAAGCTCATAGGCTGATCGA 247
QY 2427 GGAGTGTATATCATGAGGCCAAGCGGGCTTATTCTTGAGGAGATCCACCTCGTT 2486
DB 248 GGAGTGTATATCATGAGGCCAAGCGGGCTTATTCTTGAGGAGATCCACCTCGTT 307
QY 2487 GCTCACTGCATGGCGCGAAGACGCTATTGAGTGCAGATTTTCGTTGGCATATTATCG 2546
DB 308 GCTCACTGCATGGCGCGAAGACGCTATTGAGTGCAGATTTTCGTTGGCATATTATCG 367
QY 2547 CCACAAGTTACCCGACCAAGAGACCTTCATGAAAGCGGCCAAGGCCAAGTTAAGCAGAT 2606
DB 368 CCACAAGTTACCCGACCAAGAGACCTTCATGAAAGCGGCCAAGGCCAAGTTAAGCAGAT 427
QY 2607 GTTGACCCCGCTGACGCCATCTATTATTCAGAGTTGTTTCTTTGGAATGAAC 2666
DB 428 GTTGACCCCGCTGACGCCATCTATTATTCAGAGTTGTTTCTTTGGAATGAAC 487
QY 2667 TCGCTGAGGCCCATTTCTGAAGAAGATGATGATATGATATGCAATGCTGTTGCTAG 2726
DB 488 TCGCTGAGGCCCATTTCTGAAGAAGATGATGATATGATATGCAATGCTGTTGCTAG 547
QY 2727 CCAGACCAAGTCAAGGACATATGCTATTGACGCTTGACGCAATATGGAAGGTAAGTT 2786
DB 548 CCAGACCAAGTCAAGGACATATGCTATTGACGCTTGACGCAATATGGAAGGTAAGTT 607
QY 2787 GATTAATGGATCGCTCAGAGTATTTCATCCATGCGGCCCAACAGAGAACAAATTCCC 2846
DB 608 GATTAATGGATCGCTCAGAGTATTTCATCCATGCGGCCCAACAGAGAACAAATTCCC 667
QY 2847 CCAAGTTAAGCGACCGCTTTCGACCGGATTCGAAGGTCATCCGTTCCGAATGTATTAGT 2906
DB 668 CCAAGTTAAGCGACCGCTTTCGACCGGATTCGAAGGTCATCCGTTCCGAATGTATTAGT 727
QY 2907 TACGCCAGCCCTGAGCTC 2924
DB 728 TACGCCAGCCCTGAGCTC 745

RESULT 4

5428147-1
; Patent No. 5428147
; APPLICANT: BARKER, RICHARD F.; KEMP, JOHN D.
; TITLE OF INVENTION: OCTOPINE T-DNA PROMOTERS
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/91,538
; FILING DATE: 13-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 869,216
; FILING DATE: 13-APR-1992
; APPLICATION NUMBER: 869,216
; FILING DATE: 13-APR-1992
; APPLICATION NUMBER: 440,432
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 553,786
; FILING DATE: 19-NOV-1983
; APPLICATION NUMBER: 741,034
; FILING DATE: 06-AUG-1991
; APPLICATION NUMBER: 144,775
; FILING DATE: 20-JAN-1988
; APPLICATION NUMBER: 485,614
; FILING DATE: 15-APR-1983
; APPLICATION NUMBER: 713,624
; FILING DATE: 10-JUN-1991
; APPLICATION NUMBER: 260,574
; FILING DATE: 21-OCT-1988
; APPLICATION NUMBER: 848,733
; FILING DATE: 01-APR-1986
; APPLICATION NUMBER: 535,354
; FILING DATE: 26-SEP-1983
; SEQ ID NO:1:
; LENGTH: 24595
5428147-1
Query Match 23.0%; Score 733.4; DB 6; Length 24595;
Best Local Similarity 96.0%; Pred. No. 1.8e-150;
Matches 752; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 2139 TAAATCAAAATTAGAGCAAAAGTCATTCTTAACCTTCTTAAACCATGAGCCCTGCATCTAAT 2198
DB 8728 TAAATATAAAATCAGTTTGTATTCATATATCTGCAAAAACCTTATGAGCCCTGCATCTAAT 8787
QY 2199 TTTCGGTCCAACCTTGACAGGAAAGACGAGACCGCGATAGCTCTTGCCCAAGACAGAGG 2258
DB 8788 TTTCGGTCCAACCTTGACAGGAAAGACGAGACCGCGATAGCTCTTGCCCAAGACAGAGG 8847
QY 2259 GCTTCCAGTCCTTTGCTGTGATCCGGTCCATCGTGTCTCTCAACTATCAACCGGAGCGG 2318
DB 8848 GCTTCCAGTCCTTTGCTGTGATCCGGTCCATCGTGTCTCTCAACTATCAACCGGAGCGG 8907
QY 2319 ACGACCAACAGTGGAGAACTGAAAGAAAGACGAGCGCTCTTACCTTGATGATCGGCTCT 2378
DB 8908 ACGACCAACAGTGGAGAACTGAAAGAAAGACGAGCGCTCTTACCTTGATGATCGGCTCT 8967
QY 2379 GGTGAGGGTATCATCGCAGCCCAAGCAAGCTCATCATAGGCTGATCGAGGAGGTGTATAA 2438
DB 8968 GGTGAGGGTATCATCGCAGCCCAAGCAAGCTCATCATAGGCTGATCGAGGAGGTGTATAA 9027
QY 2439 TCATGAGGCCCAACGGCGGCTTATTTGAGGGAGGATCCACTCGTGTCTCAACTGCAT 2498
DB 9028 TCATGAGGCCCAACGGCGGCTTATTTGAGGGAGGATCCACTCGTGTCTCAACTGCAT 9087
QY 2499 GGGCGAAACAGCTATTGAGTGCAGATTTTCTGTCATATTAATTCGCCACAAGTTAAC 2558
DB 9088 GGGCGAAACAGCTATTGAGTGCAGATTTTCTGTCATATTAATTCGCCACAAGTTAAC 9147
QY 2559 CGACCAAGACCTTCATGAAGCGGCCAAGCCACAGAGTTAAGCAGATGTTGCAACCCCGC 2618
DB 9148 CGACCAAGACCTTCATGAAGCGGCCAAGCCACAGAGTTAAGCAGATGTTGCAACCCCGC 9207
QY 2619 TGCAGGCCATTTCTATTATTCAGAGTTGGTTTATCTTTGGAATGAACCTCGGCTGAGGCC 2678

DB 9208 TGCAGGCCATTTCTATTATTCAGAGTTGGTTTATCTTTGGAATGAACCTCGGCTGAGGCC 9267
QY 2679 CATTCTGAAAGAGATCGATGATATCGATATGCCCAGTGTGTTGCTAGCCAGAACAGAT 2738
DB 9268 CATTCTGAAAGAGATCGATGATATCGATATGCCCAGTGTGTTGCTAGCCAGAACAGAT 9327
QY 2739 CACGCAGATATGCTATTGACGCTTGACGCCAATATGAAAGTAAGTTGATTAATGGAT 2798
DB 9328 CACGCAGATATGCTATTGACGCTTGACGCCAATATGAAAGTAAGTTGATTAATGGAT 9387
QY 2799 CGCTCAGAGATATTTCATCCATGCGGCCACACAGAAAGTAATCCCCCAAGTTAACGC 2858
DB 9388 CGCTCAGAGATATTTCATCCATGCGGCCACACAGAAATCCCCCAAGTTAACGC 9447
QY 2859 AGCCGCTTTCGACGAGATTGCAAGTTCATCCGTTCCGAATGATTAAGTTACGCCAGCCCT 2918
DB 9448 AGCCGCTTTCGACGAGATTGCAAGTTCATCCGTTCCGAATGATTAAGTTACGCCAGCCCT 9507
QY 2919 GAG 2921
DB 9508 GCG 9510

RESULT 5
US-08-413-135-2
; Sequence 2, Application US/08413135
; Patent No. 5689042
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard M
; TITLE OF INVENTION: Transgenic Plants with Altered
; TITLE OF INVENTION: Senescence Characteristics
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/413,135
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 960296.92808
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 709 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "SAG12-1 Promoter DNA
; ; (truncated)"
US-08-413-135-2
Query Match 22.3%; Score 709; DB 1; Length 709;
Best Local Similarity 100.0%; Pred. No. 1.3e-145;
Matches 709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1472 AAGCTTTAACTTGACGAAATGGTTCTCTGTGAATTAACAAGATCTTGAATTCAACT 1531

QY 2666 CTGGCTGAGGCCCATCTCTGAAGAGATGATGATATCGATATGCCATGTTGTTGCTA 2725
DB 401 -----TTCTGAAGAGATCGATGATATCGATATGCCATGTTGTTGCTA 445
QY 2726 GCCAGAACGAGATCACGCGCAGATATGCTATGTCAGCTTGACGCAAAATATGGAAGTAAGT 2785
DB 446 GCCAGAACGAGATCACGCGCAGATATGCTATGCA-----GTAAGT 485
QY 2786 TGATTAATGGATCGCTCAGAGATATTCATTCATGCGGCCACACAGACAAGAAATCC 2845
DB 486 TGATTAATGGATCGCTCAGAGATATTCATTCATTCATGCGGCCACACAGACAAGAAATCC 545
QY 2846 CCCAAGTTAAGCGAGCGCGCTTCG 2869
DB 546 CCCAAGTTAAGCGAGCGCTCATCCG 569

RESULT 9
US-07-966-187-17
; Sequence 17, Application US/07966187
; Patent No. 5477001
; GENERAL INFORMATION:
; APPLICANT: SASS, Catherine
; APPLICANT: LEGUAY, Jean-Jacques
; APPLICANT: GRISON, Rene
; APPLICANT: TOPPAN, Alain
; TITLE OF INVENTION: Recombinant DNA coding for a novel
; TITLE OF INVENTION: protein having beta 1,3 glucanase activity, bacteria
; TITLE OF INVENTION: containing this DNA, transformed plant cells and plants.
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: King Street Station, Suite 500, 1800 Diagonal
; STREET: Road, PO Box 299
; CITY: ALEXANDRIA
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/966,187
; FILING DATE: 19930125
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00268
; FILING DATE: 25-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91/03588
; FILING DATE: 25-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/381
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEFAX: (703) 683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1829 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 438..1547
; FEATURE:

NAME/KEY: mat_peptide
LOCATION: 537..1547
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 438..536
US-07-966-187-17

Query Match 8.1%; Score 257.2; DB 1; Length 1829;
Best local Similarity 98.9%; Pred. No. 5.6e-47;
Matches 259; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2922 CTGCATCGTTCAACATTTGGCAATAAAGTTCTTAAGATTGAATCCTGTTGCCGCTT 2981
DB 1568 CCCGATCGTTCAACATTTGGCAATAAAGTTCTTAAGATTGAATCCTGTTGCCGCTT 1627
QY 2982 GCGATGATTCATATATATTTCTGTGAAATTAAGTAAAGCATGTAAATTAACATGTAA 3041
DB 1628 GCGATGATTCATATATATTTCTGTGAAATTAAGTAAAGCATGTAAATTAACATGTAA 1687
QY 3042 TGCATGACGTTATTTATGAGATGGTTTATGATTAGATCCCGCAATTATACATTTAA 3101
DB 1688 TGCATGACGTTATTTATGAGATGGTTTATGATTAGATCCCGCAATTATACATTTAA 1747
QY 3102 TACGCGATAGAAACAATAATATGCGCGCAAACTGGATAAATTATCGCGCGGTGTCA 3161
DB 1748 TACGCGATAGAAACAATAATATAGCGCGCAAACTAGATAAATTATCGCGCGGTGTCA 1807
QY 3162 TCTATGTTACTAGATCGAATTC 3183
DB 1808 TCTATGTTACTAGATCGAATTC 1829

RESULT 10
US-08-525-507-16
; Sequence 16, Application US/08525507
; Patent No. 5792932
; GENERAL INFORMATION:
; APPLICANT: MARCO, Yves
; APPLICANT: ROBY, Dominique
; APPLICANT: SCHNEIDER, Michel
; APPLICANT: TOPPAN, Alain
; TITLE OF INVENTION: Plant promoter, microorganisms and plant
; TITLE OF INVENTION: cells containing a unit for the expression of a protein of
; TITLE OF INVENTION: interest comprising said promoter.
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DENNISON, MESEKOLE, POLLACK & SCHREINER
; STREET: 612 Crystal Square 4 - 1745 Jefferson Davis
; STREET: Highway
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 666
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,507
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93 03299
; FILING DATE: 23-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR94/00316
; FILING DATE: 23-MAR-1994
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 412-1155
; TELEFAX: (703) 412-1161
; TELEX: 82-4412 TOWNPAT
; INFORMATION FOR SEQ ID NO: 16:

REFERENCE/DOCKET NUMBER: 16781/348
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1863 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
US-07-842-165-9

Query Match 8.1%; Score 257.2; DB 2; Length 1863;
Best Local Similarity 98.9%; Pred. No. 5.6e-47;
Matches 259; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	2922	CTCGATCGTTCACAAACATTGGCAATAAAGTTCTTAAGATTGAATCCTGTGCGGCTCTT	2981
DB	1602	CCCGATCGTTCACAAACATTGGCAATAAAGTTCTTAAGATTGAATCCTGTGCGGCTCTT	1661
QY	2982	GCGATGATTATCATATAATTTCTGTGAATTACGTTAAGCATGTAATAATTAACATGTAA	3041
DB	1662	GCGATGATTATCATATAATTTCTGTGAATTACGTTAAGCATGTAATAATTAACATGTAA	1721
QY	3042	TGCATGACGTTATTATGAGATGGGTTTTTATGATTAGATCCCGCAATTATACATTTAA	3101
DB	1722	TGCATGACGTTATTATGAGATGGGTTTTTATGATTAGATCCCGCAATTATACATTTAA	1781
QY	3102	TACGCGATAGAAAACAAATATGGCGCGCAACTGGGATAAATTATCGCGCGGTGTCA	3161
DB	1782	TACGCGATAGAAAACAAATATAGCGCCCAACTAGGATAAATTATCGCGCGGTGTCA	1841
QY	3162	TCTATGTTACTAGATCGAATTC	3183
DB	1842	TCTATGTTACTAGATCGAATTC	1863

RESULT 13

US-08-525-507-14

Sequence 14, Application US/08525507

Patent No. 5792932

GENERAL INFORMATION:

APPLICANT: MARCO, Yves

APPLICANT: ROBY, Dominique

APPLICANT: SCHNEIDER, Michel

APPLICANT: TOPPAN, Alain

TITLE OF INVENTION: Plant promoter, microorganisms and plant

TITLE OF INVENTION: cells containing a unit for the expression of a protein of

TITLE OF INVENTION: interest comprising said promoter.

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: DENNISON, MESEROLE, POLLACK & SCHEINER

STREET: 612 Crystal Square 4 - 1745 Jefferson Davis

STREET: Highway

CITY: Arlington

STATE: Virginia

COUNTRY: USA

ZIP: 666

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/525,507

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 93 03299

FILING DATE: 23-MAR-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR94/00316
FILING DATE: 23-MAR-1994
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 412-1155
TELEFAX: (703) 412-1161
TELEX: 82-4412 TOWNPAT
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 4284 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
US-08-525-507-14

Query Match 8.1%; Score 257.2; DB 1; Length 4284;
Best Local Similarity 98.9%; Pred. No. 7.1e-47;
Matches 259; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	2922	CTCGATCGTTCACAAACATTGGCAATAAAGTTCTTAAGATTGAATCCTGTGCGGCTCTT	2981
DB	4023	CCCGATCGTTCACAAACATTGGCAATAAAGTTCTTAAGATTGAATCCTGTGCGGCTCTT	4082
QY	2982	GCGATGATTATCATATAATTTCTGTGAATTACGTTAAGCATGTAATAATTAACATGTAA	3041
DB	4083	GCGATGATTATCATATAATTTCTGTGAATTACGTTAAGCATGTAATAATTAACATGTAA	4142
QY	3042	TGCATGACGTTATTATGAGATGGGTTTTTATGATTAGATCCCGCAATTATACATTTAA	3101
DB	4143	TGCATGACGTTATTATGAGATGGGTTTTTATGATTAGATCCCGCAATTATACATTTAA	4202
QY	3102	TACGCGATAGAAAACAAATATGGCGCGCAACTGGGATAAATTATCGCGCGGTGTCA	3161
DB	4203	TACGCGATAGAAAACAAATATAGCGCGCAACTAGGATAAATTATCGCGCGGTGTCA	4262
QY	3162	TCTATGTTACTAGATCGAATTC	3183
DB	4263	TCTATGTTACTAGATCGAATTC	4284

RESULT 14

US-08-673-768-1

Sequence 1, Application US/08673768

Patent No. 5952546

GENERAL INFORMATION:

APPLICANT: Bedbrook, John R.

APPLICANT: Dunsmuir, Pamela

APPLICANT: Howie, William J.

APPLICANT: Joe, Lawrence K.

APPLICANT: Lee, Kathleen Y.

TITLE OF INVENTION: Delayed Ripening Tomato Plants

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/673,768

FILING DATE: 27-JUN-1996

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000,721

FILING DATE: 30-JUN-1995

```
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 012176-005010US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15397 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-673-768-1

Query Match      8.0%; Score 256.2; DB 2; Length 15397;
Best Local Similarity 92.2%; Pred. No. 1.7e-46;
Matches 270; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

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DB 10259 GCGCAACTAGGATAAATTATCGCGCGCGGTGCATCTATGTACTAGATCGA 10311

RESULT 15
US-08-673-768-1/c
Sequence 1, Application US/08673768
Patent No. 5952546
GENERAL INFORMATION:
APPLICANT: Bedbrook, John R.
APPLICANT: Dunsmuir, Pamela
APPLICANT: Howie, William J.
APPLICANT: Joe, Lawrence K.
APPLICANT: Lee, Kathleen Y.
TITLE OF INVENTION: Delayed Ripening Tomato Plants
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,768
FILING DATE: 27-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,721
FILING DATE: 30-JUN-1995
ATTORNEY/AGENT INFORMATION:
```

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NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 012176-005010US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15397 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-673-768-1

Query Match      8.0%; Score 256.2; DB 2; Length 15397;
Best Local Similarity 92.2%; Pred. No. 1.7e-46;
Matches 270; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 2887 CCGTTCGGAATGATATTAGGTACGCCAGCCCTGAGCTCGATCGTTCAACATTGGCAAT 2946
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Search completed: June 10, 2004, 08:28:12
Job time : 255 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 10, 2004, 05:04:35 ; Search time 5033 Seconds
(without alignments)
2886.713 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 2998549 segs, 2282253817 residues

Total number of hits satisfying chosen parameters: 5997098

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3183	100.0	3183	15	US-10-072-077A-1 Sequence 1, Appli
2	733.4	23.0	1988	17	US-10-363-723-2 Sequence 2, Appli
3	730.2	22.9	2595	16	US-10-369-324-3 Sequence 3, Appli
4	730.2	22.9	2595	16	US-10-392-301-3 Sequence 3, Appli
5	730.2	22.9	2595	17	US-10-607-538-3 Sequence 3, Appli
6	730.2	22.9	9323	16	US-10-369-324-4 Sequence 4, Appli
7	730.2	22.9	9323	17	US-10-607-538-4 Sequence 4, Appli
8	714.8	22.5	723	15	US-10-187-339-12 Sequence 12, Appli
9	712.2	22.4	747	15	US-10-187-339-5 Sequence 5, Appli
10	711.8	22.4	720	16	US-10-369-493-38936 Sequence 38936, A
11	711.8	22.4	720	16	US-10-369-493-38940 Sequence 38940, A
12	711.8	22.4	720	16	US-10-369-493-38964 Sequence 38964, A
13	711.8	22.4	720	16	US-10-369-493-38966 Sequence 38966, A
14	630.2	19.8	1997	16	US-10-465-008-1 Sequence 1, Appli

15	624.4	19.6	720	16	US-10-369-493-38954	Sequence 38954, A
16	622.8	19.6	720	16	US-10-369-493-35042	Sequence 35042, A
17	622.8	19.6	720	16	US-10-369-493-38138	Sequence 38138, A
18	622.8	19.6	720	16	US-10-369-493-38549	Sequence 38549, A
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20	618	19.4	720	16	US-10-369-493-38968	Sequence 38968, A
21	601	18.9	720	16	US-10-369-493-38949	Sequence 38949, A
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24	536	16.8	723	16	US-10-369-493-38935	Sequence 38935, A
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28	262.8	8.3	7599	15	US-10-027-880-5	Sequence 5, Appli
29	261.8	8.2	4280	15	US-10-027-880-2	Sequence 2, Appli
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33	255.6	8.0	17476	15	US-10-385-546-7	Sequence 7, Appli
34	255.6	8.0	17681	15	US-10-055-001A-26	Sequence 26, Appli
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ALIGNMENTS

RESULT 1
US-10-072-077A-1
; Sequence 1, Application US/10072077A
; Publication No. US20030150009A1
; GENERAL INFORMATION:
; APPLICANT: Gallie, Daniel R.
; APPLICANT: Young, Todd E.
; TITLE OF INVENTION: The Regents of the University of California
; FILE REFERENCE: 023070-121500US
; CURRENT APPLICATION NUMBER: US/10/072, 077A
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3183
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(3183)
; OTHER INFORMATION: senescence-associated gene 12-1 (SAG12-1) promoter
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RESULT 2
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; Sequence 2, Application US/10363723
; Publication No. US20040025205A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture Victoria Services Pty Ltd
; APPLICANT: La Trobe University
; APPLICANT: SPANGENBERG, German
; APPLICANT: LIN, Yi Han
; APPLICANT: PARISH, Roger W.
; APPLICANT: Li, Song Feng W.

APPLICANT: HEAZLEWOOD, Joshua W.
; TITLE OF INVENTION: Manipulation of plant senescence
; FILE REFERENCE: 14403US
; CURRENT APPLICATION NUMBER: US/10/363, 723
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: AU PQ9946
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: PCT/AU01/01092
; PRIOR FILING DATE: 2001-06-03
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1988
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
; US-10-363-723-2

Query Match 23.0%; Score 733.4; DB 17; Length 1988;
Best Local Similarity 96.0%; Pred. No. 3.1e-125;
Matches 752; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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Db 647 TAATTAATAAATCAGTTGTATTCATATATCTGCAAAAATTTATGCACTGCATCTAAT 706
QY 2199 TTTCGCTCAACTGTCACAGGAAAGACGACGACCGCGATAGCTCTGCCAGACAGACAG 2258
| | | | |
Db 707 TTTCGCTCAACTGTCACAGGAAAGACGACGACCGCGATAGCTCTGCCAGACAGACAG 766
QY 2259 GCTTCAGTCTCTTCTGCTGATCGGGTCCAATCGTGTCTCAACTATCAACCGGAAGCG 2318
| | | | |
Db 767 GCTTCAGTCTCTTCTGCTGATCGGGTCCAATCGTGTCTCAACTATCAACCGGAAGCG 826
QY 2319 ACACCAACAGTGAAGAACTGAAGAAAGAACGACGCGTCTTAACCTTGATGATCGGCTCT 2378
| | | | |
Db 827 ACACCAACAGTGAAGAACTGAAGAAAGAACGACGCGTCTTAACCTTGATGATCGGCTCT 886
QY 2379 GGTGAGGGTATCATGCGACGCCAAGCAAGCTCATATAGCTGATCGAGAGGTGATTA 2438
| | | | |
Db 887 GGTGAGGGTATCATGCGACGCCAAGCAAGCTCATATAGCTGATCGAGAGGTGATTA 946
QY 2439 TCATGAGGCCAACGCGGGCTTAATCTTGAGGAGGATCCACTGCTCAACTGCAT 2498
| | | | |
Db 947 TCATGAGGCCAACGCGGGCTTAATCTTGAGGAGGATCCACTGCTCAACTGCAT 1006
QY 2499 GCGCGAACAAGCTATTGAGTGCAGATTTTCTGTCGATTAATTCGCCACAAGTTACC 2558
| | | | |
Db 1007 GCGCGAACAAGCTATTGAGTGCAGATTTTCTGTCGATTAATTCGCCACAAGTTACC 1066
QY 2559 CGACCAAGAGACCTTCATGAAGCGGCCAAGGCCAGAGTTAAGCAGATGTTGACCCCGC 2618
| | | | |
Db 1067 CGACCAAGAGACCTTCATGAAGCGGCCAAGGCCAGAGTTAAGCAGATGTTGACCCCGC 1126
QY 2619 TGCAGGCCATTTCTATTATCAAGAGTTGTTATCTTTGGAATGAACCTCGGCTGAGGCC 2678
| | | | |
Db 1127 TGCAGGCCATTTCTATTATCAAGAGTTGTTATCTTTGGAATGAACCTCGGCTGAGGCC 1186
QY 2679 CATTCGAAGAGATCGATGATATGATATGCCATGTTGTTGCTAGCCAGAACAGAT 2738
| | | | |
Db 1187 CATTCGAAGAGATCGATGATATGATATGCCATGTTGTTGCTAGCCAGAACAGAT 1246
QY 2739 CACGCGAGATATGCTATTGAGCTTGAAGCAATATGGAAGTAAGTTAATGGGAT 2798
| | | | |
Db 1247 CACGCGAGATATGCTATTGAGCTTGAAGCAATATGGAAGTAAGTTAATGGGAT 1306
QY 2799 CGCTCAGAGTATTTTCATCCATGCGGCCAACAGGAACAGAAATTCGCCAAGTTAACGC 2858
| | | | |
Db 1307 CGCTCAGAGTATTTTCATCCATGCGGCCAACAGGAACAGAAATTCGCCAAGTTAACGC 1366
QY 2859 AGCCGCTTGAACGATTCGAAGGTCAATCCGTTGGAATGATTAAGCTTACGCCAGCCCT 2918
| | | | |
Db 1367 AGCCGCTTGAACGATTCGAAGGTCAATCCGTTGGAATGATTAAGCTTACGCCAGCCCT 1426

QY 2919 GAG 2921
Db 1427 GCG 1429

RESULT 3

US-10-369-324-3

; Sequence 3, Application US/10369324
; Publication No. US200302213A1
; GENERAL INFORMATION:

; APPLICANT: ROMMENS, CAIUS
; APPLICANT: YE, JINGSONG
; APPLICANT: MENENDEZ-HUMARA, JAIME
; APPLICANT: YAN, HUA

; APPLICANT: RICHARD, CRAIG
; APPLICANT: BRINKERHOFF, W. LEIGH
; APPLICANT: SWORDS, KATHY M. M.

; TITLE OF INVENTION: PRECISE BREEDING
; FILE REFERENCE: 058951/0162

; CURRENT APPLICATION NUMBER: US/10/369,324
; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/357,661
; PRIOR FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: 60/377,602
; PRIOR FILING DATE: 2002-05-06

; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3
; LENGTH: 2595

; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Expression

; OTHER INFORMATION: cassette for the IPT gene
US-10-369-324-3

US-10-369-324-3

Query Match 22.9%; Score 730.2; DB 16; Length 2595;
Best Local Similarity 99.6%; Pred. No. 1.4e-124;
Matches 732; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2187 CCTGCATCTAATTTTCGGTCCAACTTGACACAGGAAGACGACCGGATAGCTCTTGC 2246
|||
Db 1166 CCTGCATCTAATTTTCGGTCCAACTTGACACAGGAAGACGACCGGATAGCTCTTGC 1225
QY 2247 CCAGCAGACAGGGCTTCCAGTCTTTCGCTTGATCGGCTCAATCGTCTCTCACTATC 2306
|||
Db 1226 CCAGCAGACAGGGCTTCCAGTCTTTCGCTTGATCGGCTCAATCGTCTCTCACTATC 1285
QY 2307 AACCGAAGCGGACGACCAAGTGAAGAACTGAAGAAAGACGCGTCTCTCACTTGA 2366
|||
Db 1286 AACCGAAGCGGACGACCAAGTGAAGAACTGAAGAAAGACGCGTCTCTCACTTGA 1345
QY 2367 TGATCGGCTCTGTGAGGGTATCATCGCAGCAAGCAAGCTCATATAGGCTGATCGA 2426
|||
Db 1346 TGATCGGCTCTGTGAGGGTATCATCGCAGCAAGCAAGCTCATATAGGCTGATCGA 1405
QY 2427 GGAAGTGTATATCATGAGGCCCAACGGCGGCTTATTCTGAGGAGAGATCCACCTCGT 2486
|||
Db 1406 GGAAGTGTATATCATGAGGCCCAACGGCGGCTTATTCTGAGGAGAGATCCACCTCGT 1465
QY 2487 GCTCACTGTCATGGCGGAAACAGCTATTTGAGTGCAGATTTTCTTGCCATATTATTCG 2546
|||
Db 1466 GCTCACTGTCATGGCGGAAACAGCTATTTGAGTGCAGATTTTCTTGCCATATTATTCG 1525
QY 2547 CCACAAGTTAACCGACCAAGAGACCTTTCATGAAAGCGGCCCAAGGCCAGATTAAAGCAGAT 2606
|||
Db 1526 CCACAAGTTAACCGACCAAGAGACCTTTCATGAAAGCGGCCCAAGGCCAGATTAAAGCAGAT 1585
QY 2607 GTTGACACCGCTGACAGGCCATTTATTTATTTCAAGAGTTGTTTATCTTTGGAATGAAC 2666
|||
Db 1586 GTTGACACCGCTGACAGGCCATTTATTTATTTCAAGAGTTGTTTATCTTTGGAATGAAC 1645
QY 2667 TCGGCTGAGGCCCATTTCTGAAGAAGATGATGATATGATATGCAATGTTGTTGCTAG 2726

Db 1646 TCGGCTGAGGCCCATTTCTGAAGAAGATGATGATATGATATGCAATGTTGTTGCTAG 1705
QY 2727 CCAGAACCAGATCACGGCAGATATGCTATTTCAGCTTGACCGGAAATATGGAAGTAACT 2786
|||
Db 1706 CCAGAACCAGATCACGGCAGATATGCTATTTCAGCTTGACCGGAAATATGGAAGTAACT 1765
QY 2787 GATTAATGGGATCGCTCAGAGATTTTCATCCATGCGCGCCCAACAGAAATTTCCC 2846
|||
Db 1766 GATTAATGGGATCGCTCAGAGATTTTCATCCATGCGCGCCCAACAGAAATTTCCC 1825
QY 2847 CCAAGTTAACGACGCCCTTTTCAGAGGATTCGAAGGTCAATCCGTTGGAATGTTAGGT 2906
|||
Db 1826 CCAAGTTAACGACGCCCTTTTCAGAGGATTCGAAGGTCAATCCGTTGGAATGTTAGGT 1885
QY 2907 TACGCCAGCCCTGAG 2921
|||
Db 1886 TACGCCAGCCCTGCG 1900

RESULT 4

US-10-392-301-3

; Sequence 3, Application US/10392301
; Publication No. US2004000343A1
; GENERAL INFORMATION:

; APPLICANT: WEEKS, J. TROY
; APPLICANT: ROMMENS, CAIUS

; TITLE OF INVENTION: REFINED PLANT TRANSFORMATION
; FILE REFERENCE: 058951/0164

; CURRENT APPLICATION NUMBER: US/10/392,301
; CURRENT FILING DATE: 2003-03-20

; PRIOR APPLICATION NUMBER: 60/365,527
; PRIOR FILING DATE: 2002-03-20

; PRIOR APPLICATION NUMBER: 60/377,597
; PRIOR FILING DATE: 2002-05-06

; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3
; LENGTH: 2595

; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cytokinin IPT

; OTHER INFORMATION: gene plasmid
US-10-392-301-3

US-10-392-301-3

Query Match 22.9%; Score 730.2; DB 16; Length 2595;
Best Local Similarity 99.6%; Pred. No. 1.4e-124;
Matches 732; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2187 CCTGCATCTAATTTTCGGTCCAACTTGACACAGGAAGACGACCGGATAGCTCTTGC 2246
|||
Db 1166 CCTGCATCTAATTTTCGGTCCAACTTGACACAGGAAGACGACCGGATAGCTCTTGC 1225
QY 2247 CCAGCAGACAGGGCTTCCAGTCTTTCGCTTGATCGGCTCAATCGTCTCTCACTATC 2306
|||
Db 1226 CCAGCAGACAGGGCTTCCAGTCTTTCGCTTGATCGGCTCAATCGTCTCTCACTATC 1285
QY 2307 AACCGAAGCGGACGACCAAGTGAAGAACTGAAGAAAGACGCGTCTCTCACTTGA 2366
|||
Db 1286 AACCGAAGCGGACGACCAAGTGAAGAACTGAAGAAAGACGCGTCTCTCACTTGA 1345
QY 2367 TGATCGGCTCTGTGAGGGTATCATCGCAGCAAGCAAGCTCATATAGGCTGATCGA 2426
|||
Db 1346 TGATCGGCTCTGTGAGGGTATCATCGCAGCAAGCAAGCTCATATAGGCTGATCGA 1405
QY 2427 GGAAGTGTATATCATGAGGCCCAACGGCGGCTTATTCTGAGGAGAGATCCACCTCGT 2486
|||
Db 1406 GGAAGTGTATATCATGAGGCCCAACGGCGGCTTATTCTGAGGAGAGATCCACCTCGT 1465
QY 2487 GCTCACTGTCATGGCGGAAACAGCTATTTGAGTGCAGATTTTCTTGCCATATTATTCG 2546
|||
Db 1466 GCTCACTGTCATGGCGGAAACAGCTATTTGAGTGCAGATTTTCTTGCCATATTATTCG 1525

QY	2547	CCACAAGTTACCCCGACCAAGAGACCTTCATGAAAGCGGCCAAGCCAGAGTTAAGCAGAT	2606
Db	1526	CCACAAGTTACCCCGACCAAGAGACCTTCATGAAAGCGGCCAAGCCAGAGTTAAGCAGAT	1585
QY	2607	GTTGCACCCCGCGTCGAGGCCATTCTATTATTCGAAGTTGGTTATCTTTGGAATGAACC	2666
Db	1586	GTTGCACCCCGCGTCGAGGCCATTCTATTATTCGAAGTTGGTTATCTTTGGAATGAACC	1645
QY	2667	TGCGCTGAGGCCCATTTCTGAAAGAGATCGATGGATATGCAATGCCATGTTGTTGCTAG	2726
Db	1646	TGCGCTGAGGCCCATTTCTGAAAGAGATCGATGGATATGCAATGCCATGTTGTTGCTAG	1705
QY	2727	CCAGAACCAGATCAAGCGCAGATATGCTATTGCAGCTTGACGCAATATGGAAGTAAGTT	2786
Db	1706	CCAGAACCAGATCAAGCGCAGATATGCTATTGCAGCTTGACGCAATATGGAAGTAAGTT	1765
QY	2787	GATTATGGGATCGCTCAGAGATATTTTCATCCATGCGGCCCAACAGGAACAGAAATPCCC	2846
Db	1766	GATTATGGGATCGCTCAGAGATATTTTCATCCATGCGGCCCAACAGGAACAGAAATPCCC	1825
QY	2847	CCAAGTTAACGCGAGCCGCTTTGCAACGGATTCGAAGGTCATCCGTTGGAATGTATTAGGT	2906
Db	1826	CCAAGTTAACGCGAGCCGCTTTGCAACGGATTCGAAGGTCATCCGTTGGAATGTATTAGGT	1885
QY	2907	TACGCCAGCCCTGAG	2921
Db	1886	TACGCCAGCCCTGCG	1900

RESULT 5
US-10-60

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; Sequence 3, Application US/10607538
; Publication No. US20040107455A1
;
; GENERAL INFORMATION:
; APPLICANT: ROMMENS, CAIUS
; APPLICANT: YE, JINGSONG
; APPLICANT: HUMARA, JAIME M.
; APPLICANT: YAN, HUA
; APPLICANT: SWORDS, KATHY
; TITLE OF INVENTION: PRECISE BREEDING
; FILE REFERENCE: 058951/0167
; CURRENT APPLICATION NUMBER: US/10/607,538
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 10/369,324
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/357,661
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/377,602
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
;
; LENGTH: 2595
;
; TYPE: DNA
;
; ORGANISM: Artificial Sequence
;
; FEATURE:
;
; OTHER INFORMATION: Description of Artificial Sequence: Expression
;
; US-10-607-538-3

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	Query Match	22.9%	Score 730.2;	DB 17;	Length 2595;
	Best Local Similarity	99.6%;	Pred. No. 1.4e-124;		
	Matches 732;	Conservative	0;	Mismatches 3;	Indels 0;
				Gaps	0;
QY	2187 CCTGCATCTAATTTTCGGTCCAACTTGACACGAAAGACGACGACCGGATAGCTCTTGC				2246
Db	1166 CCTGCATCTAATTTTCGGTCCAACTTGACACGAAAGACGACGACCGGATAGCTCTTGC				1225
QY	2247 CCAGCAGACAGGGCTTCCAGTCTTTTCGCTTGATCGGGTCCAATCGTGCTCTCAACTATC				2306
Db	1226 CCAGCAGACAGGGCTTCCAGTCTTTTCGCTTGATCGGGTCCAATGCTGTCTCAACTATC				1285

QY	2307	AACCGAAGCCGACGACCAACAGTGGAGAACTGAAAGGAACGACCGCTCTACCTTGA	2366
Db	1286	AACCGAAGCCGACGACCAACAGTGGAGAACTGAAAGGAACGACCGCTCTACCTTGA	1345
QY	2367	TGATCGGCTCTGCTGGAGGGTATCATCGGACCCAAAGCAAGCTCATATAGGCTGATCGA	2426
Db	1346	TGATCGGCTCTGCTGGAGGGTATCATCGGACCCAAAGCAAGCTCATATAGGCTGATCGA	1405
QY	2427	GGAGGTGTATATCATAGAGCCCAACGGCGGCTTATTTCTTGAGGAGGATCCACTCGTT	2486
Db	1406	GGAGGTGTATATCATAGAGCCCAACGGCGGCTTATTTCTTGAGGAGGATCCACTCGTT	1465
QY	2487	GCTCAACTGCATGGCGCGAAACAGCTATTGGAGTGCAGATTTTCGTGGCATAATTATCG	2546
Db	1466	GCTCAACTGCATGGCGCGAAACAGCTATTGGAGTGCAGATTTTCGTGGCATAATTATCG	1525
QY	2547	CCACAAGTTACCGACCAAGAGACCTTCATGAAAGCGGCCAAGGCCAGAGTTAAGCAGAT	2606
Db	1526	CCACAAGTTACCGACCAAGAGACCTTCATGAAAGCGGCCAAGGCCAGAGTTAAGCAGAT	1585
QY	2607	GTTGACCCCGCTGCAGGCCATTCTATTATTCAGAAGTTGGTTATCTTGGAAATGAACC	2666
Db	1586	GTTGACCCCGCTGCAGGCCATTCTATTATTCAGAAGTTGGTTATCTTGGAAATGAACC	1645
QY	2667	TTCGCTGAGGCCCATTTCTGAAAGAGATCGATCGATATCGATATGCCATGTTGTTGCTAG	2726
Db	1646	TTCGCTGAGGCCCATTTCTGAAAGAGATCGATCGATATCGATATGCCATGTTGTTGCTAG	1705
QY	2727	CCAGAACCAGATCAACGGCAGATATGCTATTGCACTTGACGCAATATGGAAGSTAAGTT	2786
Db	1706	CCAGAACCAGATCAACGGCAGATATGCTATTGCACTTGACGCAATATGGAAGSTAAGTT	1765
QY	2787	GATTATGGGATCGCTCAGAGTATTTTCATCCATGCGCGGCCAACAGGAACAGAAATTCCC	2846
Db	1766	GATTATGGGATCGCTCAGAGTATTTTCATCCATGCGCGGCCAACAGGAACAGAAATTCCC	1825
QY	2847	CCAAGTTAACGACGACCGCTTTGCACGGATTCGAAAGTCAATCCGTTCCGAATGTATTAAGT	2906
Db	1826	CCAAGTTAACGACGACCGCTTTGCACGGATTCGAAAGTCAATCCGTTCCGAATGTATTAAGT	1885
QY	2907	TACGCCAGCCCTGAG	2921
Db	1886	TACGCCAGCCCTGCG	1900

RESULT 6

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US-10-369-324-4
; Sequence 4, Application US/10369324
; Publication No. US2003022123A1
; GENERAL INFORMATION:
; APPLICANT: ROMMENS, CAIUS
; APPLICANT: YE, JINGSONG
; APPLICANT: MENENDEZ-HUMARA, JAIME
; APPLICANT: YAN, HUA
; APPLICANT: RICHARD, CRAIG
; APPLICANT: BRINKERHOFF, W. LEIGH
; APPLICANT: SWORDS, KATHY M. M.
; TITLE OF INVENTION: PRECISE BREEDING
; FILE REFERENCE: 058951/0162
; CURRENT APPLICATION NUMBER: US/10/369,324
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/357,661
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/377,602
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 9323
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pSIM111

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OTHER INFORMATION: nucleotide sequence
US-10-369-324-4

Query Match	22.9%	Score 730.2;	DB 16;	Length 9323;
Best Local Similarity	99.6%;	Pred. No. 2.5e-124;		
Matches 732; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

QY	2187	CCTGCATCTAATTTTTCGGTCCAACTTGCACACAGGAAAGACGACGACCGGATAGCTCTTGC	2246
Db	7646	CCTGCATCTAATTTTTCGGTCCAACTTGCACACAGGAAAGACGACGACCGGATAGCTCTTGC	7705
QY	2247	CCAGCAGACAGGGCTTCAGTCCCTTTTCGTTGATCGGGTCCAATCGTGTCTCACTATC	2306
Db	7706	CCAGCAGACAGGGCTTCAGTCCCTTTTCGTTGATCGGGTCCAATGCTGTCTCACTATC	7765
QY	2307	AACCGAAGCGAGCAGCAACAGTGAAGAAGTGAAGAAGCAAGCAGCGCTCTTACTTGA	2366
Db	7766	AACCGAAGCGGACGACCAACAGTGAAGAAGTGAAGAAGCAAGCAGCGCTCTTACTTGA	7825
QY	2367	TGATCGGCCTCTGGTGGAGGGTATCATCGCAGCCCAAGCAAGCTCATAGGCTGATCGA	2426
Db	7826	TGATCGGCCTCTGGTGGAGGGTATCATCGCAGCCCAAGCAAGCTCATAGGCTGATCGA	7885
QY	2427	GGAGGTGTATATCATGAGGCCAACGGCGGGCTTATCTTGAAGGAGATCCACCTGTT	2486
Db	7886	GGAGGTGTATATCATGAGGCCAACGGCGGGCTTATCTTGAAGGAGATCCACCTGTT	7945
QY	2487	GCTCAACTGCATGGCGCGAAAACGCTATTGGAGTGCAGATTTTCGTTGGCATATTAATCG	2546
Db	7946	GCTCAACTGCATGGCGCGAAAACGCTATTGGAGTGCAGATTTTCGTTGGCATATTAATCG	8005
QY	2547	CCACAAGTTACCCGACCAAGAGACCTTCATGAAGCGGCCAAGCCAGAGTTAAGCAGAT	2606
Db	8006	CCACAAGTTACCCGACCAAGAGACCTTCATGAAGCGGCCAAGCCAGAGTTAAGCAGAT	8065
QY	2607	GTTGCAACCCCGCTGCAGGCCATCTATTTATTCACAAGATTGGTTTATCTTTGGAATGAAC	2666
Db	8066	GTTGCAACCCCGCTGCAGGCCATCTATTTATTCACAAGATTGGTTTATCTTTGGAATGAAC	8125
QY	2667	TGCGCTGAGGCCCATTTCTGAAGAAGATCGATGGAATCGATATGCCATGTTGTGCTAG	2726
Db	8126	TGCGCTGAGGCCCATTTCTGAAGAAGATCGATGGAATCGATATGCCATGTTGTGCTAG	8185
QY	2727	CCAGAACCAGATCACGGCAGATATGCTATTGCAAGCTTGAAGCAATATGGAAGTAAAGTT	2786
Db	8186	CCAGAACCAGATCACGGCAGATATGCTATTGCAAGCTTGAAGCAATATGGAAGTAAAGTT	8245
QY	2787	GATTATGGGATCGCTCAGAGTATTTTCATCCATGCGGCCCAACAGGAACAGAAATTTCC	2846
Db	8246	GATTATGGGATCGCTCAGAGTATTTTCATCCATGCGGCCCAACAGGAACAGAAATTTCC	3305
QY	2847	CCAAAGTTAACGACGAGCCGCTTTCGACGGATTGGAAGTCAATCCGTTCCGAATGTATTAGT	2906
Db	8306	CCAAAGTTAACGACGAGCCGCTTTCGACGGATTGGAAGTCAATCCGTTCCGAATGTATTAGT	8365
QY	2907	TACGCCAGCCCTGAG 2921	
Db	8366	TACGCCAGCCCTGCG 8380	

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; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 10/369,324
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/357,661
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/377,602
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 9323
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pSIM111
; US-10-607-538-4

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Query Match	22.9%;	Score 730.2;	DB 17;	Length 9323;
Best Local Similarity	99.6%;	Pred. No. 2.5e-124;		
Matches 732; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

QY	2187	CCTGCATCTAATTTTCGGTCCAACTTGCACAGAAAGACGACGACCCGCGATAGCTCTTGC	2246
Db	7646	CCTGCATCTAATTTTCGGTCCAACTTGCACAGAAAGACGACGACCCGCGATAGCTCTTGC	7705
QY	2247	CCAGCAGACAGGGCTTCCAGTCCCTTTGCGTTGATTCGGGTCCAAATCGTGTCTCAACTATC	2306
Db	7706	CCAGCAGACAGGGCTTCCAGTCCCTTTGCGTTGATTCGGGTCCAAATGCTGTCTCAACTATC	7765
QY	2307	AACCGGAAGCGGACGACCAACAGTGAAGAAGTAAAGGAACGACGCGTCTCTAAGCTTGA	2366
Db	7766	AACCGGAAGCGGACGACCAACAGTGAAGAAGTAAAGGAACGACGCGTCTCTAAGCTTGA	7825
QY	2367	TGATCGGCTCTGCTGAGGGTATCATCGACCCAAAGCTCATCATAGGCTGATCGA	2426
Db	7826	TGATCGGCTCTGCTGAGGGTATCATCGACCCAAAGCTCATCATAGGCTGATCGA	7885
QY	2427	GGAGGTGATTAATCATAGAGCCCAACGCGCGCTATTCTTGAGGAGGATCCACTCGTT	2486
Db	7886	GGAGGTGATTAATCATAGAGCCCAACGCGCGCTATTCTTGAGGAGGATCCACTCGTT	7945
QY	2487	GCTCAACTGCATGCGCGGAAACAGCTATTGAGTGCAGATTTTCGTTGGCATTAATTGCG	2546
Db	7946	GCTCAACTGCATGCGCGGAAACAGCTATTGAGTGCAGATTTTCGTTGGCATTAATTGCG	8005
QY	2547	CCACAAGTTACCCGACCAAGAGACCTTCATGAAAGCGGCCAAGCCAGAGTTAAGCAGAT	2606
Db	8006	CCACAAGTTACCCGACCAAGAGACCTTCATGAAAGCGGCCAAGCCAGAGTTAAGCAGAT	8065
QY	2607	GTTGCACCCCGCTGCAGGCCATTCTATTATTCAAGATTGGTTATCTTTGGAATGAACC	2666
Db	8066	GTTGCACCCCGCTGCAGGCCATTCTATTATTCAAGATTGGTTATCTTTGGAATGAACC	8125
QY	2667	TCCGCTGAGGCCCATTTCTGAAGAAGATCGATGATATCGATATGCCATGTTGTTGCTAG	2726
Db	8126	TCCGCTGAGGCCCATTTCTGAAGAAGATCGATGATATCGATATGCCATGTTGTTGCTAG	8185
QY	2727	CCAGAACCCAGATCACGGCAGATATGCTATTGCGCTTGAACGCAATATGGAAGTTAAGTT	2786
Db	8186	CCAGAACCCAGATCACGGCAGATATGCTATTGCGCTTGAACGCAATATGGAAGTTAAGTT	8245
QY	2787	GATTAATGGGATCGCTCAGAGTATTTCATCCATGCGCGCCCAACAGGAACAGAAATTTCC	2846
Db	8246	GATTAATGGGATCGCTCAGAGTATTTCATCCATGCGCGCCCAACAGGAACAGAAATTTCC	8305
QY	2847	CCAAAGTTAACGACGCGCTTTCGACGCGATTTCGAAGGTATCCGTTGCGAATGTATTAGGT	2906
Db	8306	CCAAAGTTAACGACGCGCTTTCGACGCGATTTCGAAGGTATCCGTTGCGAATGTATTAGGT	8365
QY	2907	TACGCCAGCCCTGAG	2921
Db	8366	TACGCCAGCCCTGAG	8380

RESULT 8
US-10-187-339-12
; Sequence 12, Application US/10187339
; Publication No. US20030084478A1
; GENERAL INFORMATION:
; APPLICANT: Ream, Walt et al.,
; TITLE OF INVENTION: Plants Having Enhanced Gall Resistance and
; TITLE OF INVENTION: Methods and Compositions for Producing the Same
; FILE REFERENCE: 53629
; CURRENT APPLICATION NUMBER: US/10/187,339
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/434,837
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,185
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-187-339-12

Query Match 22.5%; Score 714.8; DB 15; Length 723;
Best Local Similarity 99.7%; Pred. No. 5.2e-122;
Matches 716; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2187 CCTGCATTAATTTTCGGTCCAACTTGACAGAAAGACGACCGCATAGCTCTTGC 2246
|||
DB 6 CCTGCATTAATTTTCGGTCCAACTTGACAGAAAGACGACCGCATAGCTCTTGC 65
QY 2247 CCAGCAGACAGGGCTTCCAGTCTTCCGCTTGATCGGGTCCAAATGCTCTCACTATC 2306
|||
DB 66 CCAGCAGACAGGGCTTCCAGTCTTCCGCTTGATCGGGTCCAAATGCTCTCACTATC 125
QY 2307 AACCGGAAGGAGCAGACCAACAGTGGAGAAGTGAAGAAGGACGACGGCTCTTACCTTGA 2366
|||
DB 126 AACCGGAAGGAGCAGACCAACAGTGGAGAAGTGAAGAAGGACGACGGCTCTTACCTTGA 185
QY 2367 TGATCGGCTCTGTGGAGGGTATCATCGACGCCAAGCAAGCTCATATAGGCTGATCGA 2426
|||
DB 186 TGATCGGCTCTGTGGAGGGTATCATCGACGCCAAGCAAGCTCATATAGGCTGATCGA 245
QY 2427 GGAGGTGTAATATCATGAGGCCAAGCGGGCTTATTCTTGAGGGAGATCCACCTCGTT 2486
|||
DB 246 GGAGGTGTAATATCATGAGGCCAAGCGGGCTTATTCTTGAGGGAGATCCACCTCGTT 305
QY 2487 GCTCACTGATGCGCGGGAACAGCTATTTGGAGTGCAGATTTTCGTTGGCATATTTCG 2546
|||
DB 306 GCTCACTGATGCGCGGGAACAGCTATTTGGAGTGCAGATTTTCGTTGGCATATTTCG 365
QY 2547 CCACAAGTACCCGACCAAGAGACCTTCATGAAAAGCGGCCAAGGCCAGAGTTAAGCAGAT 2606
|||
DB 366 CCACAAGTACCCGACCAAGAGACCTTCATGAAAAGCGGCCAAGGCCAGAGTTAAGCAGAT 425
QY 2607 GTTGCAACCCCGCTGCAGGCCATTTATATTCAAGAGTTGTTATCTTTGGAATGAACC 2666
|||
DB 426 GTTGCAACCCCGCTGCAGGCCATTTATATTCAAGAGTTGTTATCTTTGGAATGAACC 485
QY 2667 TCGGCTGAGGCCCATTTCTGAAGAAGATGATGATATGATATGCGATGTTGTTGCTAG 2726
|||
DB 486 TCGGCTGAGGCCCATTTCTGAAGAAGATGATGATATGATATGCGATGTTGTTGCTAG 545
QY 2727 CCAGAACCAGATCAAGGACAGATATGCTATTGCAAGCTTGACGCCAATATGAAGTAAGTT 2786
|||
DB 546 CCAGAACCAGATCAAGGACAGATATGCTATTGCAAGCTTGACGCCAATATGAAGTAAGTT 605
QY 2787 GATTATGGGATCGCTCAGAGATATTTCATCCATGCGCGCCACAGAGAAACAGAAATTCCC 2846
|||
DB 606 GATTATGGGATCGCTCAGAGATATTTCATCCATGCGCGCCACAGAGAAACAGAAATTCCC 665

RESULT 9
US-10-187-339-5
; Sequence 5, Application US/10187339
; Publication No. US20030084478A1
; GENERAL INFORMATION:
; APPLICANT: Ream, Walt et al.,
; TITLE OF INVENTION: Plants Having Enhanced Gall Resistance and
; TITLE OF INVENTION: Methods and Compositions for Producing the Same
; FILE REFERENCE: 53629
; CURRENT APPLICATION NUMBER: US/10/187,339
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/434,837
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,185
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-187-339-5

Query Match 22.4%; Score 712.2; DB 15; Length 747;
Best Local Similarity 99.6%; Pred. No. 1.6e-121;
Matches 714; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2188 CTGCATCTAATTTTCGGTCCAACTTGACAGAAAGACGACCGCATAGCTCTTGC 2247
|||
DB 18 CTGCATCTAATTTTCGGTCCAACTTGACAGAAAGACGACCGCATAGCTCTTGC 77
QY 2248 CAGCAGACAGGGCTTCCAGTCTTCCGCTTGATCGGGTCCAAATGCTCTCACTATCA 2307
|||
DB 78 CAGCAGACAGGGCTTCCAGTCTTCCGCTTGATCGGGTCCAAATGCTCTCACTATCA 137
QY 2308 ACCGGAAGCGGACGACCAACAGTGGAGAAGTGAAGAAGGACGACGGCTCTTACCTTGAT 2367
|||
DB 138 ACCGGAAGCGGACGACCAACAGTGGAGAAGTGAAGAAGGACGACGGCTCTTACCTTGAT 197
QY 2368 GATCGGCTCTGTGGAGGGTATCATCGACGCCAAGCAAGCTCATATAGGCTGATCGAG 2427
|||
DB 198 GATCGGCTCTGTGGAGGGTATCATCGACGCCAAGCAAGCTCATATAGGCTGATCGAG 257
QY 2428 GGAGGTGTAATATCATGAGGCCAAGCGGGCTTATTCTTGAGGGAGATCCACCTCGTTG 2487
|||
DB 258 GGAGGTGTAATATCATGAGGCCAAGCGGGCTTATTCTTGAGGGAGATCCACCTCGTTG 317
QY 2488 CTCACTGATGCGCGGGAACAGCTATTGGAGTGCAGATTTTCGTTGGCATATTTCG 2547
|||
DB 318 CTCACTGATGCGCGGGAACAGCTATTGGAGTGCAGATTTTCGTTGGCATATTTCG 377
QY 2548 CACAAGTACCCGACCAAGAGACCTTCATGAAAAGCGGCCAAGGCCAGAGTTAAGCAGATG 2607
|||
DB 378 CACAAGTACCCGACCAAGAGACCTTCATGAAAAGCGGCCAAGGCCAGAGTTAAGCAGATG 437
QY 2608 TTGCAACCCCGCTGCAGGCCATTTATATTCAAGAGTTGTTATCTTTGGAATGAACCT 2667
|||
DB 438 TTGCAACCCCGCTGCAGGCCATTTATATTCAAGAGTTGTTATCTTTGGAATGAACCT 497
QY 2668 CGGCTGAGGCCCATTTCTGAAGAAGATGATGATATGCGATATGCGATGTTGTTGCTAGC 2727
|||
DB 498 CGGCTGAGGCCCATTTCTGAAGAAGATGATGATATGCGATATGCGATGTTGTTGCTAGC 557
QY 2728 CAGAACCAGATCAAGGACAGATATGCTATTGCAAGCTTGACGCCAATATGAAGTAAGTTG 2787
|||
DB 558 CAGAACCAGATCAAGGACAGATATGCTATTGCAAGCTTGACGCCAATATGAAGTAAGTTG 617
QY 2788 ATTAATGGGATCGCTCAGAGATATTTCATCCATGCGCGCCACAGAGAAACAGAAATTCCC 2847

Db 618 ATTAATGGGATCGCTCAGAGTATTTCATCCATCGGCCCAACAGGACAGAAATTTCCC 577

QY 2848 CAAGTTAACGCAGCCGCTTTCGACGGATTGCAAGTCAATCCGTTGGAAATGTATTAG 2904

Db 678 CAAGTTAACGCAGCCGCTTTCGACGGATTGCAAGTCAATCCGTTGGAAATGTATTAG 734

RESULT 10
US-10-369-493-38936

```

? Sequence 38936, Application US/10369493
? Publication No. US20030233675A1
? GENERAL INFORMATION:
? APPLICANT: Cao, Yongwei
? APPLICANT: Hinkle, Gregory J.
? APPLICANT: Slater, Steven C.
? APPLICANT: Goldman, Barry S.
? APPLICANT: Chen, Xianfeng
? TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
? FILE REFERENCE: 38-10(52052)B
? CURRENT APPLICATION NUMBER: US/10/369,493
? CURRENT FILING DATE: 2003-02-28
? PRIOR APPLICATION NUMBER: US 60/360,039
? PRIOR FILING DATE: 2002-02-21
? NUMBER OF SEQ ID NOS: 47374
? SEQ ID NO 38936
? LENGTH: 720
? TYPE: DNA
? ORGANISM: Agrobacterium tumefaciens
US-10-369-493-38936

```

Query Match	22.4%;	Score 711.8;	DB 16;	Length 720;
Best Local Similarity	99.7%;	Pred. No. 1.9e-121;		
Matches 713; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	2187	CCTGCATCTAATTTTCGGTCCAACTTGCACAGGAAAGACGACGACCGGATAGCTCTTGC	2246
Db	6	CCTGCATCTAATTTTCGGTCCAACTTGCACAGGAAAGACGACGACCGGATAGCTCTTGC	65
QY	2247	CCAGCAGACAGGGCTTCCAGTCTTTCGCTTGATCGGTCCAATCGTGTCTCAACTATC	2306
Db	66	CCAGCAGACAGGGCTTCCAGTCTTTCGCTTGATCGGTCCAATCGTGTCTCAACTATC	125
QY	2307	AACCGAAGCGGACGACCAACAGTGAAGAAGTGAAGAAGACGACGCTCTACCTTGA	2366
Db	126	AACCGAAGCGGACGACCAACAGTGAAGAAGTGAAGAAGACGACGCTCTACCTTGA	185
QY	2367	TGATCGGCTCTGTTGAGGGTATCATCGCAGCCAAAGACTCATCATAGGCTGATCGA	2426
Db	186	TGATCGGCTCTGTTGAGGGTATCATCGCAGCCAAAGACTCATCATAGGCTGATCGA	245
QY	2427	GGAGGTGTATATCATGAGGCCAACGGCGGGCTTATTTCTGAGGGAAGATCCACCTCGTT	2486
Db	246	GGAGGTGTATATCATGAGGCCAACGGCGGGCTTATTTCTGAGGGAAGATCCACCTCGTT	305
QY	2487	GCTCAACTGCATGGCGCGAACAAGCTATTGGAGTGCAGATTTTCTTGGCATATTATTCG	2546
Db	306	GCTCAACTGCATGGCGCGAACAAGCTATTGGAGTGCAGATTTTCTTGGCATATTATTCG	365
QY	2547	CCACAAGTTACCCCGACCAAGAACCTTCATGAAAGCGGCCAAGCCAGAGTTAAGCAGAT	2606
Db	366	CCACAAGTTACCCCGACCAAGAACCTTCATGAAAGCGGCCAAGCCAGAGTTAAGCAGAT	425
QY	2607	GTTGCAACCCCGCTGCAGGCCATTTATTTATTTCAAGAGTTGGTTTATCTTTGGAATGAACC	2666
Db	426	GTTGCAACCCCGCTGCAGGCCATTTATTTATTTCAAGAGTTGGTTTATCTTTGGAATGAACC	485
QY	2667	TCCGCTGAGGCCCATTTCTGAAGAAGATCGATGGATATCGATATGCCATGTTGTTGCTAG	2726
Db	486	TCCGCTGAGGCCCATTTCTGAAGAAGATCGATGGATATCGATATGCCATGTTGTTGCTAG	545
QY	2727	CCAGAACCAGATCAACGCGAGATATGCTATTGCGAGCTTGACGCCAATATGGAAGTAAAGTT	2786

Db	546	CCAGAACCCAGATCACGGCAGATATGCTATTGCACTTGACCGCAATATGGAAGTAAGTT	605
QY	2787	GATTATGGGATCGCTCAGAGTATTTTCATCCATGCGCGCCCAACAGGAACAGAAATTCCC	2846
Db	606	GATTATGGGATCGCTCAGAGTATTTTCATCCATGCGCGCCCAACAGGAACAGAAATTCCC	665
QY	2847	CCAAGTTAACGCAGCCGCTTTGACGGATTGGAAGGTATCCGTTGGGAATGTAT	2901
Db	666	CCAAGTTAACGCAGCCGCTTTGACGGATTGGAAGGTATCCGTTGGGAATGTAT	720

RESULT 11
US-10-369-493-38940

```

; Sequence 38940, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 38940
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-38940

```

Query Match	22.4%	Score 711.8;	DB 16;	Length 720;
Best Local Similarity	99.7%;	Pred. No. 1.9e-121;		
Matches 713; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	2187	CCTGCATCTAATTTTTCGGTCCAACTTGCACACAGAAAGACGACGACCGGATAGCTCTTGC	2246
Db	6	CCTGCATCTAATTTTTCGGTCCAACTTGCACACAGAAAGACGACGACCGGATAGCTCTTGC	65
QY	2247	CCAGCAGACAGGGCTTCCAGTCCCTTTCGCTTGATCGGGTCCAAATCGTGTCTCAACTATC	2306
Db	66	CCAGCAGACAGGGCTTCCAGTCCCTTTCGCTTGATCGGGTCCAAATGCTGTCTCAACTATC	125
QY	2307	AACCGAAGCGGACGACCAACAGTGAAGAAGCTGAAGGAACGACGCGTCTCACTTGA	2366
Db	126	AACCGAAGCGGACGACCAACAGTGAAGAAGCTGAAGGAACGACGCGTCTCACTTGA	185
QY	2367	TGATCGGCCTCTGGTGAAGGGTATCATCGCAGCCAAAGCAAGCTCATATAGGCTGATCGA	2426
Db	186	TGATCGGCCTCTGGTGAAGGGTATCATCGCAGCCAAAGCAAGCTCATATAGGCTGATCGA	245
QY	2427	GAGGCTGTATATCATATGAGGCCCAACGGCGGCTTATTTCTGAAGGAGGATCCACCTCGTT	2486
Db	246	GAGGCTGTATATCATATGAGGCCCAACGGCGGCTTATTTCTGAAGGAGGATCCACCTCGTT	305
QY	2487	GCTCAACTGCATGGCGCGAAAACAGCTATTGGAGTGCAGATTTTCGTTGGCATATTAATTCG	2546
Db	306	GCTCAACTGCATGGCGCGAAAACAGCTATTGGAGTGCAGATTTTCGTTGGCATATTAATTCG	365
QY	2547	CCACAAGTTACCCGCAACCAAGAGACCTTCATGAAAGCGGCCAAGGCCAGAGTTAAGCAGAT	2606
Db	366	CCACAAGTTACCCGCAACCAAGAGACCTTCATGAAAGCGGCCAAGGCCAGAGTTAAGCAGAT	425
QY	2607	GTTGACACCCCGCTGACGGCCATTTCTATTATTCAGAAGTTGGTTTATCTTTGGAATGAACC	2666
Db	426	GTTGACACCCCGCTGACGGCCATTTCTATTATTCAGAAGTTGGTTTATCTTTGGAATGAACC	485
QY	2667	TCCGCTGAGGCCCATTTCTGAAGAAGATCGATGGAATCGATATGCCATGTTGTTTCTAG	2726

```
Db      486 TCGGCTGAGGCCCATTTCTGAAGAGATCGATGATATGCGATATGCCATGTGTTGCTAG 545
QY      2727 CCAGAACGAGATCACGGCAGATATGCTATTGACGCTTGACGCCAATATGGAAGTAAGTT 2786
Db      546 CCAGAACGAGATCACGGCAGATATGCTATTGACGCTTGACGCCAATATGGAAGTAAGTT 605
QY      2787 GATTATGGGATCGCTCAGGAGTATTTCATTCATGCGCGCCAAACAGAACAGAAATTCCC 2846
Db      606 GATTATGGGATCGCTCAGGAGTATTTCATTCATGCGCGCCAAACAGAACAGAAATTCCC 665
QY      2847 CCAAGTTAACGACGCCGCTTTGACGAGATTGGAAGTCAATCCGTTCCGAATGTAT 2901
Db      666 CCAAGTTAACGACGCCGCTTTGACGAGATTGGAAGTCAATCCGTTCCGAATGTAT 720
```

RESULT 12

```
US-10-369-493-38964
; Sequence 38964, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052) B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 38964
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-38964
```

```
Query Match      22.4%; Score 711.8; DB 16; Length 720;
Best Local Similarity 99.7%; Pred. No. 1.9e-121;
Matches 713; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2187 CCTGCATCTAATTTTTCGGTCCAACTTGACAGAAAGACGACCGCGATAGCTCTTGC 2246
Db      6 CCTGCATCTAATTTTTCGGTCCAACTTGACAGAAAGACGACCGCGATAGCTCTTGC 65
QY      2247 CCAGCAGACAGGGCTTCCAGTCCCTTTCGCTTGATCGGGTCCAACTGCTCTCAACTATC 2306
Db      66 CCAGCAGACAGGGCTTCCAGTCCCTTTCGCTTGATCGGGTCCAACTGCTCTCAACTATC 125
QY      2307 AACCGGAAGCGGACGACCAACAGTGAAGAACTGAAAAGAACGACGCGTCTTACCTTGA 2366
Db      126 AACCGGAAGCGGACGACCAACAGTGAAGAACTGAAAAGAACGACGCGTCTTACCTTGA 185
QY      2367 TGATCGGCTCTGTGTGAGGGTATCATCGCAGCCAAAGCAAGCTCATAGGCTGATCGA 2426
Db      186 TGATCGGCTCTGTGTGAGGGTATCATCGCAGCCAAAGCAAGCTCATAGGCTGATCGA 245
QY      2427 GGAGGTGTAATATCATGAGGCCAACGGCGGCTTATTCTTGAGGAGATCCACCTCGTT 2486
Db      246 GGAGGTGTAATATCATGAGGCCAACGGCGGCTTATTCTTGAGGAGATCCACCTCGTT 305
QY      2487 GCTCACTGCATGCGCGCGAAACAGCTATTGAGTGCAGATTTTCGTTGGCATATTATTGC 2546
Db      306 GCTCACTGCATGCGCGCGAAACAGCTATTGAGTGCAGATTTTCGTTGGCATATTATTGC 365
QY      2547 CCACAAGTTACCCGACCAAGAGACCTTCATGAAAAGCGGCCAAGGCCAGAGTTAAGCAGAT 2606
Db      366 CCACAAGTTACCCGACCAAGAGACCTTCATGAAAAGCGGCCAAGGCCAGAGTTAAGCAGAT 425
QY      2607 GTTGCACCCCGCTGCGAGGCCATTCTATTATTCAAGAGTTGTTTATTCTTTGGAATGAACC 2666
```

```
Db      426 GTTGCACCCCGCTGCGAGGCCATTCTATTATTCAAGAGTTGTTTATTCTTTGGAATGAACC 485
QY      2667 TCGGCTGAGGCCCATTTCTGAAGAGATCGATGATATGCGATATGCCATGTTGTTGCTAG 2726
Db      486 TCGGCTGAGGCCCATTTCTGAAGAGATCGATGATATGCGATATGCCATGTTGTTGCTAG 545
QY      2727 CCAGAACGAGATCACGGCAGATATGCTATTGACGCTTGACGCCAATATGGAAGTAAGTT 2786
Db      546 CCAGAACGAGATCACGGCAGATATGCTATTGACGCTTGACGCCAATATGGAAGTAAGTT 605
QY      2787 GATTATGGGATCGCTCAGGAGTATTTCATTCATGCGCGCCCAACAGAACAGAAATTCCC 2846
Db      606 GATTATGGGATCGCTCAGGAGTATTTCATTCATGCGCGCCCAACAGAACAGAAATTCCC 665
QY      2847 CCAAGTTAACGACGCCGCTTTGACGAGATTGGAAGTCAATCCGTTCCGAATGTAT 2901
Db      666 CCAAGTTAACGACGCCGCTTTGACGAGATTGGAAGTCAATCCGTTCCGAATGTAT 720
```

RESULT 13

```
US-10-369-493-38966
; Sequence 38966, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052) B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 38966
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-38966
```

```
Query Match      22.4%; Score 711.8; DB 16; Length 720;
Best Local Similarity 99.7%; Pred. No. 1.9e-121;
Matches 713; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2187 CCTGCATCTAATTTTTCGGTCCAACTTGACAGAAAGACGACCGCGATAGCTCTTGC 2246
Db      6 CCTGCATCTAATTTTTCGGTCCAACTTGACAGAAAGACGACCGCGATAGCTCTTGC 65
QY      2247 CCAGCAGACAGGGCTTCCAGTCCCTTTCGCTTGATCGGGTCCAACTGCTCTCAACTATC 2306
Db      66 CCAGCAGACAGGGCTTCCAGTCCCTTTCGCTTGATCGGGTCCAACTGCTCTCAACTATC 125
QY      2307 AACCGGAAGCGGACGACCAACAGTGAAGAACTGAAAAGAACGACGCGTCTTACCTTGA 2366
Db      126 AACCGGAAGCGGACGACCAACAGTGAAGAACTGAAAAGAACGACGCGTCTTACCTTGA 185
QY      2367 TGATCGGCTCTGTGTGAGGGTATCATCGCAGCCAAAGCAAGCTCATAGGCTGATCGA 2426
Db      186 TGATCGGCTCTGTGTGAGGGTATCATCGCAGCCAAAGCAAGCTCATAGGCTGATCGA 245
QY      2427 GGAGGTGTAATATCATGAGGCCAACGGCGGCTTATTCTTGAGGAGATCCACCTCGTT 2486
Db      246 GGAGGTGTAATATCATGAGGCCAACGGCGGCTTATTCTTGAGGAGATCCACCTCGTT 305
QY      2487 GCTCACTGCATGCGCGCGAAACAGCTATTGAGTGCAGATTTTCGTTGGCATATTATTGC 2546
Db      306 GCTCACTGCATGCGCGCGAAACAGCTATTGAGTGCAGATTTTCGTTGGCATATTATTGC 365
QY      2547 CCACAAGTTACCCGACCAAGAGACCTTCATGAAAAGCGGCCAAGGCCAGAGTTAAGCAGAT 2606
```



```
Db 366 CCACAGTACCCGACCAAGAGACCTTCATGAAAGCGGCCAGAGTTAAGCAGAT 425
QY 2607 GTTGACACCCCGTGCAGGCCCATCTTATATTCAGAGTTGGTTATCTTTGGAATGAACC 2666
Db 426 GTTGACACCCCGCTGCAGGCCCATCTTATATTCAGAGTTGGTTATCTTTGGAATGAACC 485
QY 2667 TCGGCTGAGGCCCATCTTGAAGAAGATCGATGATATCGATATGCCATGTTGTTGCTAG 2726
Db 486 TCGGCTGAGGCCCATCTTGAAGAAGATCGATGATATCGATATGCCATGTTGTTGCTAG 545
QY 2727 CCAGAACAGATCAGCGCAGATATGCTATTCAGCTTGACGCAAAATATGGAAGTAAGTT 2786
Db 546 CCAGAACAGATCAGCGCAGATATGCTATTCAGCTTGACGCAAAATATGGAAGTAAGTT 605
QY 2787 GATTATGAGATCGCTCAGAGTATTTTCATCCATGCGCGCCACACAGAAAGAAATTTCCC 2846
Db 606 GATTATGAGATCGCTCAGAGTATTTTCATCCATGCGCGCCACACAGAAAGAAATTTCCC 665
QY 2847 CCAAGTTAACGACGCCGCTTCGACGATTCGAAGTTCATCCGTTCCGAATGTAT 2901
Db 666 CCAAGTTAACGACGCCGCTTCGACGATTCGAAGTTCATCCGTTCCGAATGTAT 720
```

RESULT 14

```
US-10-465-008-1
; Sequence 1, Application US/10465008
; Publication No. US20040016016A1
; GENERAL INFORMATION:
; APPLICANT: MANKIN, LUKE S.
; APPLICANT: DA COSTA E SILVA, OSWALDO
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING PLANT PERFORMANCE
; FILE REFERENCE: 16313-0232
; CURRENT APPLICATION NUMBER: US/10/465,008
; PRIOR FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: 60/389,982
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1997
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-465-008-1
```

```
Query Match 19.8%; Score 630.2; DB 16; Length 1997;
Best Local Similarity 90.2%; Pred. No. 3.4e-106;
Matches 674; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
```

```
QY 2175 AAAACCATGACCCCTGCATCTAATTTTGGTCCAACTTGACAGAAAGACGACCGC 2234
Db 681 AAAACTTATGATCTGCTCTAATTTTGGTCCAACTTGACAGAAAGACGTCACCGC 740
QY 2235 GATAGCTCTTGCCAGACAGAGGCTTCCAGTCCCTTGCCTTGATCGGGTCCAATCGTG 2294
Db 741 GGTAGCTCTTGCCAGACAGAGGCTTCCAGTCCCTTGCCTTGATCGGGTCCAATGTTG 800
QY 2295 TCCCTCACTATCAACCGGAAGCGGACGACCAACAGTGAAGAACTGAAAGGAGACGCG 2354
Db 801 TCCCTCAGCTGTCAACCGGAAGCGGACGACCAACAGTGAAGAACTGAAAGGAGACGCCG 860
QY 2355 TCTCTAAGCTTGATGATCGGCTCTGTGTGAGGGTATCATCCAGCCAGCAAGCTCATCA 2414
Db 861 TCTTAAGCTTGATGATCGGCTCTGTGTGAGGGTATCATCCAGCCAGCAAGCTCATGA 920
QY 2415 TAGGCTGATCGAGAGGTGTATTAATCATGAGGCCAACGGCGGGCTTATTTCTTGAGGAGG 2474
Db 921 AAGGCTGATGGGGAGGTGTATTAATTAAGAGCCACGGCGGGCTTATTTCTTGAGGAGG 980
QY 2475 ATCCACCTCGTTGCTCAACTGATGCGCGGAAACAGCTAATGGAAGTGCAGATTTTCGTTG 2534
Db 981 ATCTATCTCGTTGCTCAAGTGAAGCGCGCAAGCAGTTAATGGAAGTGCAGATTTTCGTTG 1040
```

```
QY 2535 GCATATTAATTCGCCACAGATTACCCGACCAAGAGACCTTCATGAAAGCGGCCAAGGCCAG 2594
Db 1041 GCATATTAATTCGCCACAGATTACCCGACCAAGAGACCTTCATGAAAGCGGCCAAGGCCAG 1100
QY 2595 AGTTAAGCAGATGTTGCACACCCCGCTGCAGGCCCATCTTATTAATTCAGAGTTGGTTATCT 2654
Db 1101 AGTTAAGCAGATGTTAGCGCCCGCTTCAGGCCCTTCTATTAATTCAGAGTTGGTTATCT 1160
QY 2655 TTGAATGAACCTCGGCTGAGGCCCATCTTGAAGAAGATCGATGATATCGATATGCCAT 2714
Db 1161 TTGAATGAACCTCGGCTGAGGCCCATCTTGAAGAAGATCGATGATATCGATATGCCAT 1220
QY 2715 GTTGTTCCTAGCCAGAACAGATCAAGGAGATATGCTATTCAGCTTGACGCAAAATAT 2774
Db 1221 GTTGTTCCTAGCCAGAACAGATCAATCCGATATGCTATTCAGCTTGACGCAAAATAT 1280
QY 2775 GGAAGTAACTGATTAATGAGATCGCTCAGAGTATTTTCATCCATGCGGCCAACAAGA 2834
Db 1281 GGAAGTAACTGATTAATGAGATCGCTCAGAGTATTTTCATCCATGCGGCCAACAAGA 1340
QY 2835 ACAGAAATTCGCCCAAGTTAACGCGAGCGGCTTTCGACGAGATTCGAAGTTCATCCGTTCCG 2894
Db 1341 ACAGAAATTCGCCCAAGTTAACGCGAGCGGCTTTCGACGAGATTCGAAGTTCATCCGTTCCG 1400
QY 2895 AATGTATTAAGTTACGCCAGCCCTGAG 2921
Db 1401 AATGTATTAAGTTACGCCAGCCCTGAG 1427
```

RESULT 15

```
US-10-369-493-38954
; Sequence 38954, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 38954
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-38954
```

```
Query Match 19.6%; Score 624.4; DB 16; Length 720;
Best Local Similarity 92.2%; Pred. No. 2.5e-105;
Matches 658; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
```

```
QY 2188 CTGCATCTAATTTTGGTCCAACTTGACAGAAAGACGACGACCGCGATAGCTTTGCC 2247
Db 7 CTGCATCTAATTTTGGTCCAACTTGACAGAAAGACGACGACCGCGATAGCTTTGCC 66
QY 2248 CAGCAGACAGGCTTCCAGTCCCTTTCGCTTGATCGGGTCCAATCGTGTCTCACTATCA 2307
Db 67 CAGCAGACTGGGCTTCCAGTCCCTTTCGCTTGATCGGGTCCAATCGTGTCTCACTATCA 126
QY 2308 ACCGGAAGCGGACGACCAACAGTGAAGAACTGAAAGGAGCGGCTCTTAACCTTGAT 2367
Db 127 ACCGGAAGCGGACGACCAACAGTGAAGAACTGAAAGGAGCGGCTCTTAACCTTGAT 186
QY 2368 GATCGGCTCTGGTGAAGGGTATCATCCGACGCAAGCAAGCTCATAGGCTGATCGAG 2427
Db 187 GATCGGCTCTGGTGAAGGGTATCATCCGACGCAAGCAAGCTCATAGGCTGATCGAG 246
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2004, 22:11:24 ; Search time 11837 Seconds

(without alignments)
8030.018 Million cell updates/sec

Title: US-10-072-077a-1
Perfect score: 3183

Sequence: 1 gatactcttttattatca.....tatgttactagatcgaaattc 3183

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	250.2	7.9	594	29	CG408874 Des68 Ds
2	237.8	7.5	241	28	BZ382321 SALK_1181
3	216.2	6.8	628	14	CB860800 HH05G12w
4	216.2	6.8	636	14	CB861695 HH02I06w

5	210	6.6	286	28	BH854067 SALK_0786
6	168.6	5.3	311	14	CF307942 ABF_-01-J
7	168	5.3	584	12	BI807352 S104H12 S
8	155.8	4.9	547	14	CF308453 ABF_-02-E
9	150.4	4.7	688	14	CK295792 EST758506
10	150	4.7	288	12	BI807349 S104G12 S
11	137.4	4.3	222	14	CF308452 ABR_-02-E
12	130	4.1	130	28	BH854062 SALK_0786
13	121	3.8	1391	29	CG754863 P050-2-G0
14	113.6	3.6	1201	9	AL565455
15	113.6	3.6	1896	29	CG753083 P048-1-C0
16	107.6	3.4	1101	29	CNS00EVL
17	105.4	3.3	1200	13	BX415878
18	103.2	3.2	1201	9	AL565455
19	102.4	3.2	1201	29	CNS0167M
20	100.8	3.2	800	28	BH482052
21	99.2	3.1	1592	29	CG750135 P044-3-D0
22	98.8	3.1	1200	13	BX415878
23	98.8	3.1	1348	29	CG749499 P043-4-A0
24	98	3.1	405	28	BH618228
25	98	3.1	1200	13	BX437758
26	96.2	3.0	1101	29	CNS00EVL
27	95.8	3.0	1200	13	BX437758
28	95.8	3.0	1896	29	CG753083 P048-1-C0
29	92	2.9	1101	29	CNS00E07
30	91.8	2.9	1210	29	CG749728 P044-1-C0
31	91.8	2.9	1391	29	CG754863 P050-2-G0
32	90.6	2.8	1101	29	CNS00E0L
33	90.6	2.8	1626	14	CF238805
34	89.4	2.8	1101	29	CNS00E0L
35	88.4	2.8	548	28	CC055940 SALK_0980
36	87.8	2.8	1201	13	BX336467
37	87.2	2.7	1592	29	CG750135 P044-3-D0
38	87	2.7	1201	13	BX439779
39	86.4	2.7	1201	13	BX439779
40	86.2	2.7	1061	13	BX437039
41	86.2	2.7	1277	28	CC253231 CH261-180
42	86.2	2.7	1364	29	CG757970 P053-2-C0
43	86	2.7	1201	9	AL536104
44	85.8	2.7	1056	13	BX415058
45	85.8	2.7	1101	29	CNS0039G

ALIGNMENTS

RESULT 1
CG408874 594 bp DNA linear GSS 03-SEP-2003
Des68 Ds insertion lines Oryza sativa (japonica cultivar-group)
ACCESSION CG408874
VERSION CG408874
KEYWORDS genomic, genomic survey sequence.
SOURCE CG408874.1 GI:34430239
ORGANISM GSS.

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 594)

AUTHORS Kim,C.M., Piao,H.L., Park,S.J., Chon,N.S., Je,B.I., Sun,B.,
Park,S.H., Park,J.Y., Lee,E.J., Kim,M.J., Lee,J.J., Nam,M.H.,
Sun,M.Y. and Han,C.D.

TITLE Rapid, large-scale generation of Ds transposant lines and analysis
of Ds loci in rice

JOURNAL Unpublished (2003)
COMMENT Contact: Chang-deok Han
Division of Applied Life Science, PMBRC
Gyeongsang National University
Gazwa-dong 900, Jinju 660-701, South Korea
Tel: +82 55 751 6029
Fax: +82 55 759 9363
Email: cdhan@nongae.gsnu.ac.kr


```

location; chromosome 3 clone OSJNB0020011
Class: transposon-tagged.
Location/Qualifiers
1.594
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Dongjin"
/db_xref="taxon:39947"
/clone_lib="Ds insertion lines"

ORIGIN

Query Match
Best Local Similarity 7.9%; Score 250.2; DB 29; Length 594;
Matches 252; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2925 GATCGTTCAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGCTTCGCG 2984
    |||||
Db 210 GATCGTTCAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGCTTCGCG 269

QY 2985 ATGATTATCATATAATTCTGTTGAATTACGTTAAGCATGTAATAATTACATGTAATGC 3044
    |||||
Db 270 ATGATTATCATATAATTCTGTTGAATTACGTTAAGCATGTAATAATTACATGTAATGC 329

QY 3045 ATGACGTTATTTATGAGATGGGTTTTTTATGATTAGATCCCGCAATTATACATTTAATAC 3104
    |||||
Db 330 ATGACGTTATTTATGAGATGGGTTTTTTATGATTAGATCCCGCAATTATACATTTAATAC 389

QY 3105 GCGATGAAAACAAATATGCGCGCGCAAACTGGGATTAATTATCGCGCGGTGCATCT 3164
    |||||
Db 390 GCGATGAAAACAAATATAGCGCGCAAACTAGATAAATTATCGCGCGGTGCATCT 449

QY 3165 ATGTTACTAGATCGA 3179
    |||||
Db 450 ATGTTACTAGATCTA 464

RESULT 2
BZ382321 241 bp DNA linear GSS 26-NOV-2002
LOCUS BZ382321
DEFINITION SALK_118148.40.60.n Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_118148.40.60.n, genomic
survey sequence.
ACCESSION BZ382321
VERSION BZ382321
KEYWORDS BZ382321 GI:25477222
SOURCE GSS.
ORGANISM Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 241)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shim,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1.241
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"

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/clone="SALK_118148.40.60.n"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"

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ORIGIN

Query Match	7.5%;	Score 237.8;	DB 28;	Length 241;
Best Local Similarity	99.2%;	Pred. No. 3.8e-34;		
Matches 239;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

QY 1285 GAAACTTTCATAGAGATTTCAGATAGATGAAATTGGTGGGAAACATCATTTGAACAGGAAAC 1344

Db 1 GAAACTTTCATAGAGATTTCACATAGATGAAATTGGTGGGAAACATCATTTGAACAGGAAAC 60

QY 1345 TTTAGCAATCATATCGATTATCTACAAAAGAAATCTAGCGTAATGAAGTTCACCTG 1404

Db 61 TTTAGCAATCATATCGATTATCTACAAAGAAATCTAGCGTAATGAAGTTCACCTG 120

QY 1405 TTGTGAATGACTATGATTGTGATCAAAATTTAGTTAATTTTGTGCAATCATTTTCTTTTGA 1464

Db 121 TTGTGAATGACTATGATTGTGATCAAAATTTAGTTAATTTTGTGCAATCATTTTCTTTTGA 180

QY 1465 TTGATTAAGCTTTTAACCTTGACAGAAATGTTCTCTTGTGAATAAACAGAACTTTGAAT 1524

Db 181 TTGATTAAGCTTTTAACCTTGACAGAAATGTTCTCTTGTGAATAAACAGAACTTTGAAT 240

QY 1525 T 1525

Db 241 T 241

RESULT 3

CB860800/c 628 bp mRNA linear EST 22-APR-2003

LOCUS HH05G12w HH Hordeum vulgare cDNA clone HH05G12 5-PRIME, mRNA

DEFINITION sequence.

ACCESSION CB860800

VERSION CB860800.1 GI:30055359

KEYWORDS EST.

SOURCE Hordeum vulgare

ORGANISM Hordeum vulgare

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum.

1 (bases 1 to 628)

Varshney,R.K., Zhang,H., Burton,R., Stein,N., Langridge,P. and Graner,A.

TITLE Barley ESTs from coleoptile tissue

JOURNAL Unpublished (2003)

COMMENT Contact: Stein Nils

CONTACT Stein Nils

MOLECULAR MARKERS Molecular Markers Group, Department Genbank

INSTITUTE OF PLANT GENETICS AND CROP PLANT RESEARCH (IPK)

Corrensstr. 3, 06466, Gatersleben, Germany

Tel: 039482-5522

Fax: 039482-5595

Email: stein@ipk-gatersleben.de

Insert Length: 628 Std Error: 0.00

Plate: 5 row: G column: 12

Seq primer: T7.

FEATURES

Source

1.628

Location/Qualifiers

/organism="Hordeum vulgare"

/mol_type="mRNA"

/cultiivar="Sloop"

/db_xref="GABI:535262"

/db_xref="taxon:4513"

/clone="HH05G12"

/tissue_type="coleoptile"

/dev_stage="coleoptile, 1 day old"

/lab_host="DH10B"
/clone_lib="HH"
/note="Vector: pSPORT; Site 1: SalI (5-end of cDNA);
Site 2: NotI (3-end of cDNA); Due to the cloning system
used blue/white selection for recombinants is not 100 %
reliable. Average insert size is 1.3 kb."

ORIGIN

Query Match 6.8%; Score 216.2; DB 14; Length 628;
Best Local Similarity 97.7%; Pred. No. 3.2e-30;
Matches 251; Conservative 0; Mismatches 3; Indels 3; Gaps 3;
QY 2922 CTCGATCGTTCAACACATTGGCAATAAGTTCTTAAGATTGAATCCTGTTGCCGCTT 2981
Db 264 CCCGATCGTTCAACACATTGGCAATAAGTTCTTAAGATTGAATCCTGTTGCCGCTT 206
QY 2982 GCGATGATTATCATATAATTCTGTTGAATTACGTTAAGCATGTAATAATTACATGTAA 3041
Db 205 GCGATGATTATCATATAATTCTGTTGAATTACGTTAAGCATGTAATAATTACATGTAA 146
QY 3042 TGCATGACGTTATTATGAGATGGTTTTATGATTAGATCCCGCAATTATACATTTAA 3101
Db 145 TGCATGA-GTTATTATGAGATGGTTTTATGATTAGATCCCGCAATTATACATTTAA 87
QY 3102 TACGCGATAGAAAACAAATATAGCGCGCAAACTGGATAAATTATCGCGCGGTGTCA 3161
Db 86 TACGCGATAGAAAAC-AAATATAGCGCGCAAACTAGATAAATTATCGCGCGGTGTCA 28
QY 3162 TCTATGTTACTAGATCG 3178
Db 27 TCTATGTTACTAGATCG 11

RESULT 4

LOCUS CB861695/c 636 bp mRNA linear EST 22-APR-2003
DEFINITION HH02106w HH Hordeum vulgare cDNA clone HH02106 5-PRIME, mRNA
ACCESSION CB861695
VERSION CB861695
KEYWORDS CB861695.1 GI:30056254
SOURCE EST.
ORGANISM Hordeum vulgare
Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 636)
AUTHORS Varshney,R.K., Zhang,H., Burton,R., Stein,N., Langridge,P. and Graner,A.
TITLE Barley ESTs from coleoptile tissue
JOURNAL Unpublished (2003)
COMMENT Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 636 Std Error: 0.00
Plate: 2 Row: I Column: 6
Seq primer: T7.

FEATURES

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Location/Qualifiers
/organism="Hordeum vulgare"
/mol_type="mRNA"
/cultivar="Sloop"
/db_xref="GABI:534665"
/db_xref="taxon:4513"
/clone="HH02106"
/tissue_type="coleoptile"
/dev_stage="coleoptile, 1 day old"
/lab_host="DH10B"
/clone_lib="HH"

/note="Vector: pSPORT; Site 1: SalI (5-end of cDNA);
Site 2: NotI (3-end of cDNA); Due to the cloning system
used blue/white selection for recombinants is not 100 %
reliable. Average insert size is 1.3 kb."

ORIGIN

Query Match 6.8%; Score 216.2; DB 14; Length 636;
Best Local Similarity 97.7%; Pred. No. 3.2e-30;
Matches 251; Conservative 0; Mismatches 3; Indels 3; Gaps 3;
QY 2922 CTCGATCGTTCAACACATTGGCAATAAGTTCTTAAGATTGAATCCTGTTGCCGCTT 2981
Db 260 CCCGATCGTTCAACACATTGGCAATAAGTTCTTAAGATTGAATCCTGTTGCCGCTT 202
QY 2982 GCGATGATTATCATATAATTCTGTTGAATTACGTTAAGCATGTAATAATTACATGTAA 3041
Db 201 GCGATGATTATCATATAATTCTGTTGAATTACGTTAAGCATGTAATAATTACATGTAA 142
QY 3042 TGCATGACGTTATTATGAGATGGTTTTATGATTAGATCCCGCAATTATACATTTAA 3101
Db 141 TGC-TGACGTTATTATGAGATGGTTTTATGATTAGATCCCGCAATTATACATTTAA 83
QY 3102 TACGCGATAGAAAACAAATATAGCGCGCAAACTGGATAAATTATCGCGCGGTGTCA 3161
Db 82 TACGCGATAG-AAACAAATATAGCGCGCAAACTAGATAAATTATCGCGCGGTGTCA 24
QY 3162 TCTATGTTACTAGATCG 3178
Db 23 TCTATGTTACTAGATCG 7

RESULT 5

LOCUS BH854067 286 bp DNA linear GSS 13-JUN-2002
DEFINITION SALK_078693.24.40.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_078693.24.40.x, genomic
survey sequence.
ACCESSION BH854067
VERSION BH854067.1 GI:21424938
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 286)
AUTHORS Alonso,J.M., Leisese,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
JOURNAL Arabidopsis Genome
COMMENT Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.

FEATURES

source 1. .286
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_078693.24.40.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was


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QY      3056 TATGATGGGTTTATTATGATTAGAGTCCCGCAATTATACATTTAATACGCGATAGAAAA 3115
      |||||||
Db      433 TATGATGGGTTTATTATGATTAGAGTCCCGCAATTATACATTTAATACGCGATANGAAA 492

QY      3116 CAAAATATGGCGCGCAAACTGGGATAAT 3144
      |||||||
Db      493 ACAAATATAGCGCCAAACTAGATAAAAT 521

RESULT 8
CF308453/c      547 bp      mRNA      linear      EST 15-AUG-2003
LOCUS
DEFINITION      ABF--02-E14.g1 ABF3-overexpressing transgenic rice plasmid cDNA
ACCESSION      CF308453
VERSION      CF308453
KEYWORDS      CF308453.1 GI:33680214
SOURCE      EST.
ORGANISM      Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharoidae; Oryzae; Oryza.
REFERENCE      1 (bases 1 to 547)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
TITLE      Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
JOURNAL      Large-scale Sequencing Analysis of Rice ESTs
COMMENT      Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: hnahm@ggbio.com, hnahm@bio.myongji.ac.kr.

FEATURES
Source
1..547
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--02-E14"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

ORIGIN
Query Match      4.9%; Score 155.8; DB 14; Length 547;
Best Local Similarity 98.7%; Pred. No. 6e-19;
Matches 157; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2922 CTCGATCGTCAACACATTTGGCAATAAAGTTCTTAAGATTGAATCCTGTGCGGCTCT 2981
      |||||||
Db      174 CCGGATCGTCAACACATTTGGCAATAAAGTTCTTAAGATTGAATCCTGTGCGGCTCTT 115

QY      2982 GCGATGATTATCATATAATTTCTGTGAATTACGTTAAGCATGTAATAATTAACATGTAA 3041
      |||||||
Db      114 GCGATGATTATCATATAATTTCTGTGAATTACGTTAAGCATGTAATAATTAACATGTAA 55

QY      3042 TGCATGACGTTATTATGAGATGGGTTTATGATTAGA 3080
      |||||||
Db      54 TGCATGACGTTATTATGAGATGGGTTTATGATTAGA 16

RESULT 9
CK295792/c      284 bp      mRNA      linear      EST 15-DEC-2003
LOCUS
DEFINITION      CK295792.1 GI:39880533
ACCESSION      CK295792
VERSION      CK295792
KEYWORDS      CK295792.1 GI:39880533
SOURCE      EST.
ORGANISM      Nicotiana benthamiana
Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE      1 (bases 1 to 284)
AUTHORS      Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
TITLE      Staskiewicz,B., Jin,H. and Baker,B.
JOURNAL      Generation of EST sequences from Nicotiana benthamiana
COMMENT      Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: GTA ATA CGA CTC ACT ATA GGG C.

FEATURES
Source
1..284
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NBMCX34"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: PCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN
Query Match      4.7%; Score 150.4; DB 14; Length 284;
Best Local Similarity 99.3%; Pred. No. 7.1e-18;
Matches 151; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2922 CTCGATCGTCAACACATTTGGCAATAAAGTTCTTAAGATTGAATCCTGTGCGGCTCT 2981
      |||||||
Db      152 CTCGATCGTCAACACATTTGGCAATAAAGTTCTTAAGATTGAATCCTGTGCGGCTCTT 93

QY      2982 GCGATGATTATCATATAATTTCTGTGAATTACGTTAAGCATGTAATAATTAACATGTAA 3041
      |||||||
Db      92 GCGATGATTATCATATAATTTCTGTGAATTACGTTAAGCATGTAATAATTAACATGTAA 33

QY      3042 TGCATGACGTTATTATGAGATGGGTTTAT 3073
      |||||||
Db      32 TGCATGACGTTATTATGAGATGGGTTTAT 1

RESULT 10
BI807349/c      688 bp      mRNA      linear      EST 02-OCT-2001
LOCUS
DEFINITION      S104G12 Stem library from Oryza sativa (3-5 leaf stage) Oryza
ACCESSION      BI807349
VERSION      BI807349
KEYWORDS      BI807349.1 GI:15854553
SOURCE      EST.
ORGANISM      Oryza sativa
Oryza sativa
```

```
QY      3056 TATGATGGGTTTATTATGATTAGAGTCCCGCAATTATACATTTAATACGCGATAGAAAA 3115
      |||||||
Db      433 TATGATGGGTTTATTATGATTAGAGTCCCGCAATTATACATTTAATACGCGATANGAAA 492

QY      3116 CAAAATATGGCGCGCAAACTGGGATAAT 3144
      |||||||
Db      493 ACAAATATAGCGCCAAACTAGATAAAAT 521

RESULT 8
CF308453/c      547 bp      mRNA      linear      EST 15-AUG-2003
LOCUS
DEFINITION      ABF--02-E14.g1 ABF3-overexpressing transgenic rice plasmid cDNA
ACCESSION      CF308453
VERSION      CF308453
KEYWORDS      CF308453.1 GI:33680214
SOURCE      EST.
ORGANISM      Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharoidae; Oryzae; Oryza.
REFERENCE      1 (bases 1 to 547)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
TITLE      Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
JOURNAL      Large-scale Sequencing Analysis of Rice ESTs
COMMENT      Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: hnahm@ggbio.com, hnahm@bio.myongji.ac.kr.

FEATURES
Source
1..547
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--02-E14"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

ORIGIN
Query Match      4.9%; Score 155.8; DB 14; Length 547;
Best Local Similarity 98.7%; Pred. No. 6e-19;
Matches 157; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2922 CTCGATCGTCAACACATTTGGCAATAAAGTTCTTAAGATTGAATCCTGTGCGGCTCT 2981
      |||||||
Db      174 CCGGATCGTCAACACATTTGGCAATAAAGTTCTTAAGATTGAATCCTGTGCGGCTCTT 115

QY      2982 GCGATGATTATCATATAATTTCTGTGAATTACGTTAAGCATGTAATAATTAACATGTAA 3041
      |||||||
Db      114 GCGATGATTATCATATAATTTCTGTGAATTACGTTAAGCATGTAATAATTAACATGTAA 55

QY      3042 TGCATGACGTTATTATGAGATGGGTTTATGATTAGA 3080
      |||||||
Db      54 TGCATGACGTTATTATGAGATGGGTTTATGATTAGA 16

RESULT 9
CK295792/c      284 bp      mRNA      linear      EST 15-DEC-2003
LOCUS
DEFINITION      CK295792.1 GI:39880533
ACCESSION      CK295792
VERSION      CK295792
KEYWORDS      CK295792.1 GI:39880533
SOURCE      EST.
ORGANISM      Nicotiana benthamiana
Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE      1 (bases 1 to 284)
AUTHORS      Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
TITLE      Staskiewicz,B., Jin,H. and Baker,B.
JOURNAL      Generation of EST sequences from Nicotiana benthamiana
COMMENT      Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: GTA ATA CGA CTC ACT ATA GGG C.

FEATURES
Source
1..284
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NBMCX34"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: PCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN
Query Match      4.7%; Score 150.4; DB 14; Length 284;
Best Local Similarity 99.3%; Pred. No. 7.1e-18;
Matches 151; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2922 CTCGATCGTCAACACATTTGGCAATAAAGTTCTTAAGATTGAATCCTGTGCGGCTCT 2981
      |||||||
Db      152 CTCGATCGTCAACACATTTGGCAATAAAGTTCTTAAGATTGAATCCTGTGCGGCTCTT 93

QY      2982 GCGATGATTATCATATAATTTCTGTGAATTACGTTAAGCATGTAATAATTAACATGTAA 3041
      |||||||
Db      92 GCGATGATTATCATATAATTTCTGTGAATTACGTTAAGCATGTAATAATTAACATGTAA 33

QY      3042 TGCATGACGTTATTATGAGATGGGTTTAT 3073
      |||||||
Db      32 TGCATGACGTTATTATGAGATGGGTTTAT 1

RESULT 10
BI807349/c      688 bp      mRNA      linear      EST 02-OCT-2001
LOCUS
DEFINITION      S104G12 Stem library from Oryza sativa (3-5 leaf stage) Oryza
ACCESSION      BI807349
VERSION      BI807349
KEYWORDS      BI807349.1 GI:15854553
SOURCE      EST.
ORGANISM      Oryza sativa
Oryza sativa
```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 688)
Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X.,
Wu, H.F., Jiang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.
A Gene Expression Screen in Oryza sativa
Unpublished (2001)
Contact: Haitao Dong, Debao Li
Bioinformatics and Gene Network Research Group
Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86892051
Fax: 0086-571-86961525
Email: webmaster@estarray.org, URL: http://www.estarray.org
Seq primer: M13 forward primer.

FEATURES
source

1. 688
/organism="Oryza sativa"
/mol_type="mRNA"
/db_xref="taxon:4530"
/clone="S104G12"
/tissue_type="Stem"
/dev_stage="3-5 leaf stage"
/clone_lib="Stem library from Oryza sativa (3-5 leaf
stage)"
/note="Vector: pSport2"

ORIGIN

Query Match 4.7%; Score 150; DB 12; Length 688;
Best Local Similarity 93.8%; Pred. No. 6.8e-18;
Matches 167; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 2968 CTGTTGCCGCTTCGGATGATATATATTTCTGTGAATTACGTTAAGCATGTAA 3027
|||
Db 623 CCGTGTGCGGCTCGCATGATTATCATATATTTCTGTGAATTACGTTAAGCATGTAA 564
QY 3028 TAATTAACATGTAATGATGACGCTATTATGAGATGGGTTTATGATTAAGATCCCGC 3087
|||||
Db 563 TAATTAACATGTAATGATGACGCTATTATGAGATGGGTTTATGATTAAGATCCCGC- 505
QY 3088 AATTATACATTTAATAACGCGATAGAAAAACAAAATATGGCGCGCAACTGGGATTAATT 3145
|||||
Db 504 AATTATACATTTAATAACGCGATAGAAAAACAAAATATAGCGCGCAACTGATTAATAAT 447

RESULT 11
CF308452 222 bp mRNA linear EST 15-AUG-2003
LOCUS ABE--02-E14.b1 ABEF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa cDNA clone ABE--02-E14, mRNA sequence.
ACCESSION CF308452
VERSION CF308452.1 GI:33680213
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 222)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

1. 222
Location/Qualifiers

/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--02-E14"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

ORIGIN

Query Match 4.3%; Score 137.4; DB 14; Length 222;
Best Local Similarity 99.3%; Pred. No. 2e-15;
Matches 138; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2922 CTCGATCGTCAACACATTGGCAATAAAGTTTCTTAAGATTGAATCCTGTCGGGCTT 2981
|||
Db 84 CCCGATCGTCAACACATTGGCAATAAAGTTTCTTAAGATTGAATCCTGTCGGGCTT 143
QY 2982 GCGATGATATCATATATTTCTGTGAATTACGTTAAGCATGTAATAATTAACATGTAA 3041
|||||
Db 144 GCGATGATATCATATATTTCTGTGAATTACGTTAAGCATGTAATAATTAACATGTAA 203
QY 3042 TGCATGACGTTATTATGA 3060
|||
Db 204 TGCATGACGTTATTATGA 222

RESULT 12
BH854062 130 bp DNA linear GSS 13-JUN-2002
LOCUS SALK_078685.53.75.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_078685.53.75.x, genomic
survey sequence.
ACCESSION BH854062
VERSION BH854062.1 GI:21424933
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 130)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.

FEATURES
source

1. 130
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_078685.53.75.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

Query Match	4.1%;	Score 130;	DB 28;	Length 130;
Best Local Similarity	100.0%;	Pred. No. 5.5e-14;		
Matches 130; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

DY 1366 TATCTACAAAAGATACTTAGCGTAATGAAGTTCACTTGTTGTAATGACTATGATTGGA 1425
|||
Dd 61 TATCTACAAAAGATACTTAGCGTAATGAAGTTCACTTGTTGTAATGACTATGATTGGA 120

Qy	1426	TCAAATTAGT	1435
Db	121	TCAAATTAGT	130

RESULT 13	CG754863	LOCUS	CG754863	1391 bp	DNA	linear	GSS 24-OCT-2003
DEFINITION	P050-2-G05.za	Ppa EcoRI	BAC Library	Pristionchus	pacificus	genomic,	genomic survey sequence.

ORIGIN

Query Match	3.88;	Score 121;	DB 29;	Length 1391;
Best Local Similarity	44.88;	Pred. No. 1.5e-12;		
Matches 496;	Conservative 0;	Mismatches 608;	Indels 3;	Gaps 3;

OY		790	GAGGTGATTGTGATTTAAATTGGTGA	CTAGGGCGAATCCTTCACATCACAAATAACAAGT	849
Dδ		285	GGGGGGGGGCTNTTNTTNTTNTTNTT	TTTTTNNNNTTTTTTNTTAAATTTTTTTT	344

QY	850	TTTATGATTTTTTTTATACATTTTGGCACCCTTCGTAAGTTGGTATTTACACCG	909
Db	345	TTNNNTTTTTTTTAACTTTNNNTTTTTTTTTTTTTTTTTTTTTTTTTTTT	404
QY	910	CATTTTCCCTGACAGAATTCATATATTATTTATATACTCCAGTTGACAATTAT	969
Db	405	TTTTTTTTTTTTTTNNNTTNNNTTTTTTTTTTTTTTTTTNNNTTTTTTTTTTTT	464

OY 970 AAGTTATAACGTTTTTACAATTATTTAAATACCATGTGAAGATCCAGAATATGCTTAA 1025
| | | | | | | | | | | | | | | | | | |
Db 465 TTTTTTTTAAATTTTAAATTTTATTTAATAATATTAATTTTATTAATTAATAATAT 524

QY	1030	CTTCTTCTTGTGTAAGAAACTA	CTATATACCTTAATPAAATAAT	TCTTAATCATAT	10895
Db	525	ATTATTTTATTATTAATATTA	TATTAATTAATTAATAATTA	AAAAATTAATAATATTA	584

QY 1090 ATTTGTAATATGACGTTATTTGTCAAATTTGAAATTTAGATTTTAGACGGTTATCACTT 1145
| | | | | | | | | | | | | | | | | |
Db 585 AATTAATATTAATAATANAATATATATATTTATNATATATATATTTTAAATATATATTTTT 644

Qy	1150	CAGCCAATATGATTGGATTTAAGTCCAAAANGCAATTTCGTACGTAT-CCCTCTTGC	1208
Db	645	ATTAAATTTATTAATTTTATATATAATTAATATTTAAATTTNATANAAAAATATATATTAATTTAATT	704

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QY      1209 GTCATGATTATTCATATTTCTATATTACCCTAACAAGAGCTACATTATATT 1268
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      705 TTTTATATATATTTTAAATTAATATTTATTTAAATAAAAATTAATATTAATTAAT 764

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OY      1269 GTATTCTAATGACAGGAAACTTTCATAGAGATTGAGATAGATGAATTTGGTGGGAACA 1328
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      765 AATTATTAAATAAAAAAATTTTTTTTAAATTATTAATTTTATATATTTATATTT 824

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QY 1329 TCATTGAACAGGAAACTTTTTCGCAATCATATCGATTTATCTACAAAAGAATACTTAGCG 1388
| | | | | | | | | |
Db 825 ATTTTATATTTTATTTATTTATTAATAATATATTTTATTTTATTAATTAATATTTAAT 884

QY 1389 TAATGAAGTTCACCTTGTTGTGAATGACTATGATTGCAAATTAGTTAATTTTGCGAA 1448

DB 885 TTTTATAATTAATAATTNTTATTATTATTTTTTTTTTTTATTATATTATTATTAAT 944

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QY      1449 TCATTTTCCTTTTGATTGATTAAGCTTTTAACTTGACCGAATGGTCTCTGTGAATA 1508
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      945 ATATAATTTTAAATTAAATTTTAAATTATAPAAATTNTTATANTTTATTAATAAAAAATA 1004

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QY      1509 AACAGATCTTTGATTCAACTATTGTAGTGAAGAAAAGACAAAGAAGATTCCTTGTT    1568
          |   |||   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      1005 TATTANTAATTNTAATAATAATATTTAAAAATATATANATTTAAAAAATTAATAATTTTT    1064

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QY 1569 TTTATGTGATTGATTTTGGTCATGAAGTAACCTAAGTACTACAAGAAAAATAAAC 1628

DJ 1065 ATTAATATATPAAAAATATTTAATTATATATAAATTAATTATTTATATAAATTAATTAATAA 1124

QY 1629 ATGTACGTAACGTATCAGCATGTAAAGATTTTTTCCAAATATTATACCTATG 1688

DB 1125 ATATA-TTAAATNTTTTATTATTNAAATTAATATATATAATATTTAAATTTTA 1183

QY 1689 ATAGATTTTTTTTGAATGTCATTAAAAATGCTTCTTAATATTAAATT 1748
||| ||| ||| | ||| ||| ||| ||| |||
Db 1184 ATATATTATTATAAATAATATATTAAAAATAATTTTATATATATTTAAAAATT 1243

DY 1749 AATTAATAAGAAATATATTATGCAAAACATCATCAACATATCCAACTTGGAAAAT 1808

Ddb 1244 AANPAATAATTATTTATTTATATATTTATTTAATTATAAATAAATAAATAATT 1303

QY 1809 CTCTATAGTACACAGTAGAGAATAATTACTAGATACAACTTCCATATCTCAA 1868

Ddb 1304 TTAAATATATAATAATTA-ATTATATATATATATATTAATTAAATAATTAAATAATTAAT 1362

QY 1869 TTATAATGTTACAAACCTAATTAA 1895
| | | | |
Db 1363 AATAATAATTNTAAATATTTAATAAA 1389

RESULT	14
LOCUS	AL565455
DEFINITION	AL565455 Homo sapiens FETAL BRAIN Homologous to mouse CSODF005Y018 3-PRIME, mRNA sequence.
ACCESSION	AL565455
VERSION	AL565455.2 GI:30549492
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1201) Li, W.-B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001) On Feb 16, 2001 this sequence version replaced gi:12916848.
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

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FEATURES
source      Location/Qualifiers
1: .1201

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QY	1365	CTACAAAAGAAATCTAGCGGTAATGAAGTTCACCTGTTGTGAATGACTATGATTGATCA	1428
Db	678	ATAWATAWATAWATATATAWATAWATAWATAWATAWATAWATAWATAWATAWATAW	737
QY	1429	AATTAGTTAATTTTGTGGAATCATTTTCTTTGATTGATTAAGCTTTAACTTGAC	1488
Db	738	ATAWATAWATAWATATATAWATAWATAWATAWATAWATAWATAWATAWATAWATAW	797
QY	1489	GAATGTTCTCTTGTGAATAAACAGAACTCTTGAATTCAAACTATTGATTAGTGAAG	1548
Db	798	ATAWATAWATAWATATATAWATAWATAWATAWATAWATAWATAWATAWATAWATAW	857
QY	1549	ACAAAAGAAGATTCCTGTTTATGTGATTAGATTTTGATGCATGAAGGTAAC	1608
Db	858	ATAWATAWATAWATATATAWATAWATAWATAWATAWATAWATAWATAWATAWATAW	917
QY	1609	GTACTACAAGAAAATAAACATGTACGTAACGATCCAGCATGTAAGATTTTTTT	1668
Db	918	ATAWATAWATAWATATATAWATAWATAWATAWATAWATAWATAWATAWATAWATAW	977
QY	1669	CCAAATAATTTTACTCATGATAGATTTTTTTTTTGAATGTCAATTTAAATGCTTT	1728
Db	978	ATAWATAWATAWATATATAWATAWATAWATAWATAWATAWATAWATAWATAWATAW	1037
QY	1729	CTTAATATTTAATTTTAATTTAATTAATAAGGAATATATTTATGCAAAAACATCAAC	1788
Db	1038	ATAWATAWATAWATATATAWATAWATAWATAWATAWATAWATAWATAWATAWATAW	1097
QY	1789	ACATATCCAACCTTGGAAAATCTCTATAGTACACAAGTAGAGAAAAATAAATTTACTAGAT	1848
Db	1098	ATAWATAWATAWATATATAWATAWATAWATAWATAWATAWATAWATAWATAWATAW	1157
QY	1849	ACAAACTTCCTTAATCATCAATTATAAATGTTTACAAAATAATT	1892
Db	1158	ATAWATAWATAWATATATAWATAWATAWATAWATAWATAWATAWATAWATAWATAW	1201

RESULT 15
CG753083
LOCUS
DEFINITION
CG753083 1896 bp DNA linear GSS 24-OCT-2003
P048-1-C01.za Ppa ECORI BAC Library Pristionchus pacificus genomic,
genomic survey sequence.
ACCESSION
CG753083
VERSION
CG753083.1 GI:37977199
KEYWORDS
GSS.
SOURCE
Pristionchus pacificus
ORGANISM
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
1 (bases 1 to 1896)
Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
AUTHORS
An integrated physical and genetic map of the nematode Pristionchus
TITILE
pacificus
JOURNAL
Mol. Genet. Genomics 269 (5), 715-722 (2003)
MEDLINE
22835951
PUBMED
12884007
COMMENT
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.

